

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 11:05:26 ; Search time 25 Seconds

(without alignments)
541.530 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARGMERWRDLALVTGAS.....STPAHIQIGDIQMPTEQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331.5	24.8	248	1	YDFG_SALTY
2	329.5	24.6	248	1	YDFG_ECOLI
3	317.5	23.7	252	1	YDFG_HAEIN
4	314.5	23.5	238	1	YDXD_BACSU
5	295	22.1	251	1	Y484_MYCTU
6	293	21.9	267	1	YW71_YEAST
7	287.5	21.5	245	1	NODG_RHIS3
8	278.5	20.8	249	1	SDH_AGRU
9	278	20.8	259	1	YQJQ_BACSU
10	275.5	20.6	249	1	SDH_AGRU
11	271.5	20.3	246	1	FABG_BACSU
12	269	20.1	246	1	FABG_THENA
13	269	20.1	248	1	Y432_LISMO
14	269	20.1	248	1	Y452_LISIN
15	269	20.1	260	1	NDG4_BOVIN
16	268.5	20.1	245	1	NODG_RHIME
17	267.5	20.0	320	1	FABG_CUPLA
18	258.5	19.3	244	1	FABG_VIBCH
19	251	18.8	260	1	DHS4_RABIT
20	249.5	18.7	261	1	ACT3_STROO
21	248	18.5	260	1	DHS4_PIG
22	246	18.4	260	1	DHS4_HUMAN
23	245.5	18.4	244	1	FABG_VIBHA
24	244	18.2	260	1	DHS4_MOUSE
25	243	18.2	261	1	DHG2_BACME
26	239	17.9	247	1	FAG1_SYNY3
27	239	17.9	260	1	DHS4_RAT
28	238.5	17.8	244	1	FABG_BUCAL
29	238.5	17.8	244	1	FABG_EUCAP
30	238	17.8	248	1	Y4EK_RHISN
31	237.5	17.8	272	1	DHK1_STRVN
32	237.5	17.8	319	1	FABG_ARATH
33	237.5	17.8	336	1	T52_MAIZE

34	236.5	17.7	244	1	CBR2_MOUSE
35	236	17.7	246	1	PBBB_CHRVI
36	236	17.7	249	1	BA71_EUBSP
37	235.5	17.6	253	1	Y945_MYCTU
38	234.5	17.5	244	1	CBR2_PIG
39	234	17.5	256	1	BUDC_KLEPN
40	232	17.4	248	1	PHAB_ACISP
41	230.5	17.2	248	1	FABG_AQUAE
42	230.5	17.2	287	1	HEIN_ANASP
43	229	17.1	261	1	DHGA_BACME
44	229	17.1	271	1	SDR1_PICAB
45	228.5	17.1	278	1	Y4LA_RHISN

ALIGNMENTS

RESULT 1

ID	YDFG_SALTY	STANDARD;	PRT;	248 AA.
AC	P40864;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Hypothetical oxidoreductase ydfg (EC 1.-.-.-).			
GN	YDFG OR STM1511 OR STY1550 OR T1432.			
OS	Salmonella typhimurium, and			
OS	Salmonella typhi.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Salmonella.			
OX	NCBI_TaxID=602, 601;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;			
RX	MEDLINE=21534948; PubMed=11677609;			
RA	McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,			
RA	Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,			
RA	Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,			
RA	Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,			
RA	Waterston R., Wilson R.K.;			
RT	"Complete genome sequence of Salmonella enterica serovar Typhimurium			
RT	LT2.";			
RL	Nature 413:852-856(2001).			
RN	[2]			
RP	SEQUENCE OF 1-97 FROM N.A.			
RC	SPECIES=S.typhimurium;			
RX	MEDLINE=92165738; PubMed=1537804;			
RA	Miller C.G., Hamilton S.;			
RA	"Cloning and nucleotide sequence of the Salmonella typhimurium dcp			
RT	gene encoding dipeptidyl carboxypeptidase.";			
RL	J. Bacteriol. 174:1626-1630(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=S.typhi; STRAIN=CT18;			
RX	MEDLINE=21534947; PubMed=11677608;			
RA	Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,			
RA	Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,			
RA	Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,			
RA	Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,			
RA	Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,			
RA	Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,			
RA	Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,			
RA	Whitehead S., Barrall B.G.;			
RT	"Complete genome sequence of a multiple drug resistant Salmonella			
RT	enterica serovar Typhi CT18.";			
RL	Nature 413:848-852(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;			
RX	MEDLINE=22531367; PubMed=12644504;			
RA	Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,			
RA	Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;			
RT	"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2			

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RT and CTL8." ;
RN J. Bacteriol. 185:2330-2337 (2003).
RL [5]
RP IDENTIFICATION.
RX SPECIES=S.typhimurium;
MEDLINE=95004589; PubMed=7920643;
RA Robison K., Gilbert W., Church G.M.;
RT "Large scale bacterial gene discovery by similarity search.";
CC Nat. Genet. 7:205-214 (1994).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY. STRONG, TO OTHER BACTERIAL HOMOLOGS.
CC -----
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CC -----
DR EMBL; AE008766; AAL20430.1; -.
DR EMBL; M84575; -; NOT_ANNOTATED_CDS.
DR EMBL; AL627270; CAD01802.1; -.
DR EMBL; AE016838; AAO69074.1; -.
DR StyGene; SG10499; ydfg.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh_short_1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP BIND 4 28 NAD OR NADP (BY SIMILARITY).
FT ACT SITE 147 147 BY SIMILARITY.
FT FT 56 70 RNAAIEEMMASLPA -> QPRGHRDDGLSAS (IN
FT FT REF. 2).
SQ SEQUENCE 248 AA; 27043 MW; A99FEC9188EFC8E4 CRC64;

Query Match 24.8%; Score 331.5; DB 1; Length 248;
Best Local Similarity 35.1%; Pred. No. 8.3e-21;
Matches 87; Conservative 112; Indels 13; Gaps 56

QY 13 LALVTGASGIGGAARVALVOQGLKVVGCAATVGNIEELAAECKSAGYPTGLIPYRCDLS 72
Db 2 IIVLTGATGEGCIARFVENGHKVATGRRHRIQLAKDELGE-----NVLTQAQLDVR 56
QY 73 NEEDILSMFSAIRSHSGVDVICINNAGLARP-DTLLSGSTSGWKMDNFNVNVALSICTR 131
Db 57 NRAAIEEMASLPQWRDIDVLVNNAGLGLGEPAAKASVEDWETMTIDTNKGLIYMTRA 116
QY 132 AYQSMKERNVDDGHIININSMGHRVLPVLTHTFYSATKVAATVLTBGLRQELREAQTHI 191
Db 117 VLPGMVERN--RGHIINIGTAGS--WPYAGGNVYGATKAFVRQFSINLRTDLH--GTAV 170
QY 192 RATCISPGVW-ETQFAFKLHDKDEKAAATVEQMKLKPEDVAEAVIYVLSTPAHIQIGD 250
Db 171 RVTDIEPLGVGIEFSSVRFGKDDKAGKIYENTALTPEDIETAVWVATLPAHVNIINT 230
QY 251 IQMRPTEQ 258
Db 231 VENMPVTQ 238

RESULT 2
YDFG_ECOLI
ID YDFG_ECOLI STANDARD; PRT; 248 AA.
AC P39831; P77149; P78161; P78162;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable oxidoreductase ydfg (EC 1.-.-.-).
OS ydfg or B1539.
GN Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

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KW	Oxidoreductase; Complete proteome.	
NP BIND	4	28
FT	147	NAD OR NADP (BY SIMILARITY).
ACT SITE	147	BY SIMILARITY.
FT	182	G -> T (IN REF. 3).
CONFLICT	182	
SEQUENCE	248 AA;	6FECC5FBAA86EA42 CRC64;
Query Match	24.6%;	Score 329.5; DB 1; Length 248;
Best local Similarity	35.9%;	Pred. No. 1.2e-20;
Matches	89; Conservative	34; Mismatches 112; Indels 13; Gaps 6;
QY	13	LALVTGASGGIGAAVARALVQGLKVVGCARTVGNIEELAAECKSAGYGGTLIPYRCOLS 72
DB	2	IVLVGTAGTAGGECITRRFQQGHKVTATGRQRLOELKDELGNLYAOL-----DVR 56
QY	73	NEEDILSMFSAIRSOHSGVDICINNAGIA-RPDTLLSGSTSGWKDMFNVNVLALSICTRE 131
DB	57	NRAAIEEMLASLPAEWCNIDILVNNAGIALGMEPAHKASVEDWETMIDTNNKGLVYMTRA 116
QY	132	AYQSMKERNVDDGHIININMSGHRVLPVLSVTHFYSA TKYAVTALTGLRQELREAO THI 191
DB	117	VLPQMWERN--HGHIINIGTAGS--WPYAGGNVYGATKAPVRQFSLNRLTDLH--GTAV 170
QY	192	RATCISPGVV-ETQFAFKLHDKPEKAAATYBQMKCLKPEDVSAVIVLSTPAHIQIGD 250
DB	171	RVTDIEELGVGTGETFSNVRFGDDGKAEKTYQNTALTPEPDSAVVMVSTLPAHVINT 230
QY	251	IQMRPTEQ 258
DB	231	LEMVFTQ 238
RESULT 3		
YDFG	HAEIN	STANDARD; PRT; 252 AA.
ID	YDFG	HAEIN
AC	P45200;	
DT	01-NOV-1995	(Rel. 32, Created)
DT	01-NOV-1995	(Rel. 32, Last sequence update)
DE	28-FEB-2003	(Rel. 41, Last annotation update)
DE	Hypothetical oxidoreductase HI1430	(EC 1.-.-.-).
GN	HI1430.	
OS	Haemophilus influenzae.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;	
OC	Pasteurellaceae; Haemophilus.	
OX	NCBI_TaxID=727;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Rd / KW20 / ATCC 51907;	
RC	MEDLINE=95350630; Pubmed=7542800;	
RX	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,	
RA	Kerlavage A.R., Bult C.J., Tomb J.-P., Dougherty B.A., Merrick J.M.,	
RA	McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,	
RA	Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,	
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,	
RA	Utterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,	
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,	
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,	
RA	Venter J.C.;	
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae	
RT	Rd";	
RL	Science 269:496-512(1995).	
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES	
CC	(SDR) FAMILY. STRONG, TO OTHER BACTERIAL HOMOLOGS.	
CC		
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CC		
DR	EMBL; U32822; AAC23077.1; -.	
DR	PIR; H64122; H64122.	

Db 224 PRFI 228

RESULT 5

Y484 MYCTU STANDARD; PRT; 251 AA.

ID Y484 MYCTU STANDARD; PRT; 251 AA.

AC Q11150;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Putative oxidoreductase RV0484c/MT0502 (EC 1.-.-.-).

GN RV0484C OR MT0502 OR MTCV20G9.10C.

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

NCBI_TaxId=1773;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=H37RV;

RC MEDLINE=98295987; PubMed=9634230;

RX Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Teklaia F., RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R., RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G., RA "Deciphering the biology of Mycobacterium tuberculosis from the RT complete genome sequence.";

RL Nature 393:537-544 (1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CDC 1551 / OshKosh;

RX MEDLINE=22206494; PubMed=1218036;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., RA Peterson J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A., RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;

RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and RT laboratory strains.";

RL J. Bacteriol. 184:5479-5490(2002).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY. STRONG, TO BACTERIAL YDFG HOMOLOGS.

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DR EMBL; Z77162; CAB00945.1; --

DR EMBL; AE006951; AAK4725.1; --

DR PIR; G70743; G70743.

DR HSSP; P14061; 1FDU.

DR TIGR; MT0502; --

DR Tuberculist; RV0484c; --

DR InterPro; IPR002198; ADH_short.

DR Pfam; PF00106; adh_short_1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; FALSE_NEG.

KW Hypothetical protein; Oxidoreductase; Complete proteome.

FT NP BIND 12 36 NAD OR NADP (BY SIMILARITY).

FT ACT SITE 149 149 BY SIMILARITY.

SQ SEQUENCE 251 AA; 26416 MW; 6F3956B95DB92BA2 CRC64;

Query Match 22.1%; Score 295; DB 1; Length 251;

Best Local Similarity 34.3%; Pred. No. 1e-17;

Matches 87; Conservative 43; Mismatches 102; Indels 22; Gaps 8;


```

Db 7 RKAUVTGASGGIGEAIRALRVLAHQ-AIVLHGTRVEKLETLAAE---LGRDVKLPP--AN 60
Qy 71 LSNBEDIILSMFAIRSOHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTR 130
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LSNRDEVKALQKAEADLEGVDILVNNAGITKGLFVRMSDADWDVLEVNLTAVFRULTR 120
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 131 EAYQSMKERNVDDGHHIININSMGHRVLPUSVTHFYSAKYAVTALTSLGRLQELBEAQTH 190
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 ELTHPMRMR--HGRRIINITSVVGVTGNPGQTN--YCASKAGMIGFSGSLAQEI--ATRN 174
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 191 IRATCISPGVVEVTFQAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSPTA 244
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 ITVNCVARGFIESAMTKLNDKQKAEIMAAIPTREMGTSVEVASAVIASNEA 228
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
SDH_AGRU
ID SDH_AGRU STANDARD; PRT; 249 AA.
AC Q9KWN1;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Serine 3-dehydrogenase (EC 1.1.1.276).
GN SDH.
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=356;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR1600;
RX MEDLINE=22087129; PubMed=12092831;
RA Fujisawa H., Nagata S., Chowdhury E.K., Matsumoto M., Misono H.;
RT "Cloning and sequencing of the serine dehydrogenase gene from
RT Agrobacterium tumefaciens.";
RL Biosci. Biotechnol. Biochem. 66:1137-1139(2002).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=97179806; PubMed=9028042;
RA Chowdhury E.K., Higuchi K., Nagata S., Misono H.;
RT "A novel NADP(+)-dependent serine dehydrogenase from Agrobacterium
RT tumefaciens.";
RL Biosci. Biotechnol. Biochem. 61:152-157(1997).
CC -!- FUNCTION: Catalyzes the oxidation of the hydroxyl group of serine
CC to form 2-aminomalate semialdehyde which is spontaneously
CC converted into 2-aminoacetaldehyde and CO(2). Also acts on D-
CC serine, L-glycerate, D-glycerate and 2-methyl-DL-serine. Does not
CC act on O-methyl-DL-serine and L-threonine.
CC -!- CATALYTIC ACTIVITY: L-serine + NADP(+) = 2-aminomalate
CC semialdehyde + NADPH.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
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CC EMBL; AB032242; BAB07807.1; -.
DR PIR; JC7857; JC7857.
DR HSSP; Pf4061; IFDU.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR TIGRFAMs; TIGR01831; fabg rel; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP.
FT NP_BIND 6 30 NADP (BY SIMILARITY).
FT ACT_SITE 148 148 BY SIMILARITY.

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```

SQ SEQUENCE 249 AA; 26745 MW; 5DCE3C404C950BDA CRC64;
Query Match 20.8%; Score 278.5; DB 1; Length 249;
Best Local Similarity 29.7%; Pred. No. 2.5e-16;
Matches 74; Conservative 45; Mismatches 109; Indels 21; Gaps 7;
Qy 15 LVTGASGGIGAAVARALVQGLKVVGCAARTVGNTEELAAECKSAGYPTLLPYRCDLSNE 74
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LITGATGFGGATQAFKVEGKVGITGRRARLEALSALGSA-FHGVAF---DITDE 60
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 75 EDILSMFAIRSOHSGVDICINNAGLA-----RPTLLSGSTSGWKDMFNVNVLALSICT 129
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 EATKALAGLPGDFRIDILVNNAGLAGTAPAPQVPL---KQQTWVDNITGLLNV 116
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 130 REAYQSMKERNVDDGHHIININSMGHRVLPUSVTHFYSAKYAVTALTSLGRLQELBEAQ 189
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 HHLPLTLIERK---GIVINLSSVAAH--YPLVGGNVYGTFAFLRQFSLGRSDIHL--GK 169
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 190 HIRATCISPGVVEVTFQAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSPTAHIQIG 249
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 GVRVTSIEPGMCETEFTLVRTGGQASDNLYKGNPITADDIANTIHVASQPKHININ 229
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 250 DIQMRPTEQ 258
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 SLELMPVQ 238
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
YQJQ_BACSU
ID YQJQ_BACSU STANDARD; PRT; 259 AA.
AC P54554;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical oxidoreductase yqjQ (EC 1.-.-.-).
GN YQJQ OR BSU23780.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=97124195; PubMed=8969508;
RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
RA Kobayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
RT the Bacillus subtilis genome containing the skin element and many
RT sporulation genes.";
RL Microbiology 142:3103-3111(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Boursier M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriello R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,

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Qy 190 HIRATCISPGVVETQFAFKLHDKDEKAAATYEQMKLKPEDVAEAVIYVLSTPAHIQIG 249
Db 170 GVRVTSIEPGMCETEFTLVRTGNGQASDNLKYGVPNTADDIANTIIYVVASQPKHIN 229
Qy 250 DIQMRPTQ 258
Db 230 SLELMPVQ 238

RESULT 11
FABG_BACSU STANDARD; PRT; 246 AA.
AC P51831; 031733;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR BSU15910.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96326321; PubMed=8759840;
RA Morbidoni H.R., de Mendoza D., Cronan J.B. Jr.;
RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
RT lipid biosynthesis genes.";
RL J. Bacteriol. 178:4794-4800(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Bruillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Enitan K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA Frits G., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-172 FROM N.A.
RC STRAIN=168;
RX MEDLINE=98195738; PubMed=9534248;
RA Foulger D., Errington J.;
RT "A 28 kbp segment from the spoVM region of the Bacillus subtilis 168
RT genome.";
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RL Microbiology 144:801-805(1998).
RN [4]
RP SEQUENCE OF 230-246 FROM N.A.
RC STRAIN=168;
RA Oguro A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC 1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC 1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC 1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U59433; AAC44307.1; -
DR EMBL; Z99112; CAB13464.1; -
DR EMBL; Y13937; CRA74250.1; -
DR EMBL; D64116; BAA10974.1; -
DR PIR; A69621; A69621.
DR HSSP; Q12634; 1YBV.
DR Subtilist; BG11535; fabg.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; FALSE NEG.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 9 33 NADP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
FT CONFLICT 23 23 D -> A (IN REF. 1).
SQ SEQUENCE 246 AA; 26282 MW; C6A391167D3237DC CRC64;

Query Match 20.3%; Score 271.5; DB 1; Length 246;
Best Local Similarity 32.9%; Pred. No. 9.4e-16;
Matches 82; Conservative 38; Mismatches 10; Indels 27; Gaps 10;

Qy 11 DRLAVTGASGGIGAAVARALVQGLKVVGCAVTGN---IEELAAECKSAGYPTGLIPY 67
Db 4 DKTAIVTGASRGIGRSIALDLAKSGANVV--VNYSGNEAKANEVVDKSMGRKA--IAV 59
Qy 68 RCDLSNEEDILSMFSATRSQHSQVDICINAGLARPDTLLSGSTSGWKDMFNVLALS 127
Db 60 KADVSNPEDVQNMKETLSVFSTIDILVNNAGITRDNLIMRMKEDWDVNIINLKGVFN 119
Qy 128 CTRE-AYOSMKERNVDDGHIININSMGSHRVLPVLSVTHFYSAKYAVTALTEGLRQELRE 186
Db 120 CTKAVTROMMKQRS---GRINVSIVGVSGNPGQAN--YVAAKAGVTLTKSSAKEL-- 172
Qy 187 AQTHIRATCISPGVVETQFAFKLHDKDEKAAATYEQMKCL-----KPEDVAEAVIYVL 240
Db 173 ASRNTVNAIAPGGFISTDMTKL-AKQVQD-----EMLKQIPLARFGPSDVSSVVTFLA 226
Qy 241 STPAHIQIG 249
Db 227 SEGARYMTG 235

RESULT 12
FABG_THEMA STANDARD; PRT; 246 AA.
AC Q9X248;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
OS Thermotoga maritima.
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OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=9287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RL genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -!- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC -----
CC EMBL; AE001811; AAD36790.1; -.
CC DR PIR; H72219; H72219.
CC DR HSSP; P50162; 1AB1.
CC DR TIGR; TM1724; -.
CC DR InterPro; IPR002198; ADH_short.
CC DR Pfam; PF00106; adh_short; 1.
CC DR PRINTS; PR00080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH_SHORT; 1.
CC DR Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
CC KW NP BIND 10 34 NADP (BY SIMILARITY).
CC FT ACT_SITE 154 154 BY SIMILARITY.
CC SQ SEQUENCE 246 AA; 26401 MW; 8C08904D28099142 CRC64;

Query Match 20.1%; Score 269; DB 1; Length 246;
Best Local Similarity 28.2%; Pred. No. 1.5e-15;
Matches 69; Conservative 54; Mismatches 112; Indels 10; Gaps 5;

Qy 8 RWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGYPTLIPY 67
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 RLEGKVLITGAASGIGKATLLFAQEGATVIAGDISKENLDSLVKEAE--GLPGKVDPY 59
Qy 68 RCDLSNEEDILSMFSAIRSQHSQGVDDICINNAGLARPDPTLLSGSTSGWKDMFNVALSI 127
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
60 VLNVTRDQIKVEVKVQKGRIDLVLNNAGITRDALLVMKEEDMDAVINVLKGVFN 119
Qy 128 CTREAYOSM_KERNVDDGHIININSMGSHRVLPLSVTHFYFSATKYAVTALTEGLRQELRE 186
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 VTQMVVPMLIKQRN--GSIYVSVSVGIYGNPQTN--YAASKAGVIGMTKTWAKEL-- 172
Qy 187 AQTHIRATCTSPGVVETQFAKLHDKDPEKAAAYEQMKLKPEDVAEAVIYVLSTPAHI 246
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
173 AGNRINRVAVAPGFIETPMTEKLPEKARETALSRPLGRFGKPEEVAQVILFLASDESSY 232
Qy 247 QIGDI 251
Db 233 VTQGV 237

RESULT 13
Y432_LISMO
ID Y432_LISMO STANDARD; PRT; 248 AA.
AC P25145;
DT 01-MAY-1992 (Rel. 22, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase Lmc0432 (EC 1.-.-.-) (ORFA).
GN LMC0432.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD / Serovar 1/2a;
RX MEDLINE=91292517; PubMed=1905979;
RA Galliard J.-L., Berche P., Frehel C., Gouin E., Cossart P.;
RT "Entry of L. monocytogenes into cells is mediated by internalin, a
RT repeat protein reminiscent of surface antigens from Gram-positive
RT cocci.";
RL Cell 65:1127-1141(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC -----
CC EMBL; M67471; AAA25288.1; -.
CC DR EMBL; AL591975; CAC98511.1; -.
CC DR PIR; A1128; A1128.
CC DR HSSP; O70351; 1E6W.
CC DR ListList; LMO00432; -.
CC DR InterPro; IPR002198; ADH_short.
CC DR Pfam; PF00106; adh_short; 1.
CC DR PRINTS; PR00080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH_SHORT; 1.
CC DR Hypothetical protein; Oxidoreductase; Complete proteome.
CC KW NP BIND 9 33 NAD OR NADP (BY SIMILARITY).
CC FT ACT_SITE 154 154 BY SIMILARITY.
CC FT CONFLICT 48 48 T -> I (IN REF. 1).
CC FT CONFLICT 182 182 V -> A (IN REF. 1).
CC SQ SEQUENCE 248 AA; 26821 MW; 50262487D29FD935 CRC64;

Query Match 20.1%; Score 269; DB 1; Length 248;
Best Local Similarity 27.5%; Pred. No. 1.5e-15;
Matches 70; Conservative 51; Mismatches 116; Indels 18; Gaps 4;

Qy 10 RDRLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGYPTLIPYRC 69
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 KKKVITITGASSGIGKATALLAEKGAKLVLAAARRVEKLEKIVOTIKANS--GEAIFAKT 61
Qy 70 DLSNEEDILSMFSAIRSQHSQGVDDICINNAGLARPDPTLLSGSTSGWKDMFNVALSI 123
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 DVTKREDNKKVLAEIERYKGVDAIFLNAIGMPNPLSALKDEDEWEQMDINIKVLNGI 121
Qy 124 ALSTCTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYFSATKYAVTALTEGLRQ 183

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Db      122 AAVLPSTFAQKS-----GHIATSSVAGLKAYPGGAV--YGATKWAVRDLMEVLRME 171
QY      184 LREAQTHIRATCISPGVVETQFAFKLHDKDPKAAATYEQMKLKPEDVAEAVIIVLSTP 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      172 SAQEGTNRITATYPAAINTELLETTIDKETEQGMNTLYKQGVTPDRIASIVAYAIQDP 231
QY      244 AHIQIGDIQMRPTEQ 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      232 EDVNNFTVGTQTSQ 246

RESULT 14
Y452 LISIN
ID Y452 LISIN STANDARD; PRT; 248 AA.
AC Q92EK7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase Lin0452 (EC 1.-.-.-).
GN Lin0452.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI TaxID:1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fshiz H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Coseart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -! SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
      (SDR) family.
CC
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CC
CC EMBL; AL596165; CAC95684.1; -.
CC F1R; AD1489; AD1489.
CC ListList; LIN00452; -.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP BIND 9 33 NAD OR NADP (BY SIMILARITY).
FT ACT SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 248 AA; 26808 MW; EAE7EB01F110306F CRC64;

Query Match 20.1%; Score 269; DB 1; Length 248;
Best Local Similarity 27.8%; Pred. No. 1.5e-15;
Matches 71; Conservative 50; Mismatches 116; Indels 18; Gaps 4;

QY 10 RDRALVTGASGGIGAAVARALVQGLKVVGGARTVGNTEELAAECKSAGYPTLIPYRC 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 KKKVLIITGASSGIGETAILLAEGKALVLAARVEKLEKIVQTIKASS--GEAIFAKT 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 DLISNEEDILMSFSAIRKSHQSGVDICINNAGLARPDTLTLLSGSTSGWKMDPNVNV-----L 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      62 DVTKEEDNKLVELAIERYGVKDAIFLNAGIMPNSPLSALKDEDEWEQIMDINIKGVNLGI 121
QY      124 ALSICTREAYOSMKERNVDDGHIININSMGSHRVLPISVTHFYSATKYAVTALTGLRQE 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      122 AAVLPSTFAQKS-----GHIATSSVAGLKAYPGGAV--YGATKWAVRDLMEVLRME 171
QY      184 LREAQTHIRATCISPGVVETQFAFKLHDKDPKAAATYEQMKLKPEDVAEAVIIVLSTP 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      172 SAQEGTNRITATYPAAINTELLETTIDKETEQGMNTLYKQGVTPDRIASIVAYAIQDP 231
QY      244 AHIQIGDIQMRPTEQ 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      232 EDVNNFTVGTQTSQ 246

RESULT 15
DHS4 BOVIN
ID DHS4 BOVIN STANDARD; PRT; 260 AA.
AC Q8SPU8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Dehydrogenase/reductase SDR family member 4 (EC 1.1.1.184) (NADPH-
DE dependent carbonyl reductase/NADP-retinol dehydrogenase) (CR) (PBCR)
DE (Peroxisomal short-chain alcohol dehydrogenase) (NADPH-dependent
DE retinol dehydrogenase/reductase) (NDRD).
GN DHS4 OR NDRD.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Wang G.L., Liu G.F., Du J., Xu X.L., Gasana V., Wang B., Zhu L.,
RA Huang D.Y.;
RT "Bos taurus NDRD mRNA for NADPH-dependent retinol
RT dehydrogenase/reductase.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Reduces all-trans-retinol and 9-cis retinol. Can also
CC catalyze the oxidation of all-trans-retinol with NADP as co-
CC factor, but with much lower efficiency. Reduces alkyl phenyl
CC ketones and alpha-dicarbonyl compounds with aromatic rings, such
CC as pyrimidine 4-aldehyde, 3-benzoylpyridine, 4-benzoylpyridine,
CC menadione and 4-hexanoylpyridine. Has no activity towards
CC aliphatic aldehydes and ketones (By similarity).
CC -! CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.
CC -! SUBUNIT: Homotrimer (By similarity).
CC -! SUBCELLULAR LOCATION: Peroxisomal (By similarity).
CC -! MISCELLANEOUS: Inhibited by kaempferol, quercetin, genistein and
CC myristic acid (By similarity).
CC -! SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
      (SDR) family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF487454; AAL93248.1; -.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Peroxisome.
FT NP BIND 18 42 NADP (BY SIMILARITY).
FT SITE 258 260 MICROBODY TARGETING SIGNAL.
SQ SEQUENCE 260 AA; 27385 MW; F76610B3EF128C3D CRC64;

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Query Match 20.1%; Score 269; DB 1; Length 260;
Best Local Similarity 31.2%; Pred. No. 1.6e-15;
Matches 81; Conservative 51; Mismatches 106; Indels 22; Gaps 10;

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Db	1	MASCGMARPNLDNKVALVTASTDGGIFAIRRLAQDGAHVVSRRKQNVDRAVATLKG	60	
QY	58	AG--YPGTLIPYKCDLSNEEDILSMESAIRSQHSQVDICINNAGLARP--DTLLSGSTSG	113	
Db	61	EGLSVTGTV----	CHVGKAEDRRLVATAVKLHGGVDILISNAAVS-PFFGSLMDVPEEV	115
QY	114	WKDMFNVNVALSICTREAYQSMKERNVDDGHIININSMGHRVLPVSVTHFYSAKYAV	173	
Db	116	WDKILDVNVKATALLTKAVVPEMAKRG--GGSIVIVSSIAAYS--PFPSLGPYNVSKTAL	171	
QY	174	TALTEGLROELREAOQHIRATCISPGVETQFAFKLHDKDP---EKAATYEQMKCLKPE	230	
Db	172	LGLTKNLALEL--AESNVVNCLAPGLINTSFSLWE-DPARQESIKATFQIKRIGKPE	228	
QY	231	DVAEAVIYVLSTPAHIQIGD	250	
Db	229	ECAGIVSFLCSEDAASYITGE	248	

Search completed: September 15, 2004, 11:26:35
Job time : 27 secs

B/a < K

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 11:26:12 ; Search time 52 Seconds

(without alignments)
1603.448 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMERWRDLALVTGAS.....STPAHQIGDIQMRPTEQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pap.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1337	100.0	260	9	US-09-796-089-1	Sequence 1, Appli
2	1337	100.0	260	12	US-10-206-915-378	Sequence 378, App
3	1337	100.0	260	12	US-10-199-670-378	Sequence 378, App
4	1337	100.0	260	12	US-10-201-858-378	Sequence 378, App
5	1337	100.0	260	12	US-10-205-890-378	Sequence 378, App
6	1337	100.0	260	12	US-10-208-024-378	Sequence 378, App
7	1337	100.0	260	12	US-10-201-853-378	Sequence 378, App
8	1337	100.0	260	12	US-10-063-745-128	Sequence 128, App
9	1337	100.0	260	12	US-10-063-512-128	Sequence 128, App
10	1337	100.0	260	12	US-10-063-513-128	Sequence 128, App
11	1337	100.0	260	12	US-10-063-515-128	Sequence 128, App
12	1337	100.0	260	12	US-10-063-549-128	Sequence 128, App
13	1337	100.0	260	12	US-10-063-569-128	Sequence 128, App
14	1337	100.0	260	12	US-10-063-551-128	Sequence 128, App
15	1337	100.0	260	12	US-10-174-581-378	Sequence 378, App

16	1337	100.0	260	12	US-10-176-483-378	Sequence 378, App
17	1337	100.0	260	12	US-10-176-749-378	Sequence 378, App
18	1337	100.0	260	12	US-10-176-914-378	Sequence 378, App
19	1337	100.0	260	12	US-10-176-915-378	Sequence 378, App
20	1337	100.0	260	12	US-10-063-555-128	Sequence 128, App
21	1337	100.0	260	12	US-10-063-563-128	Sequence 128, App
22	1337	100.0	260	12	US-10-063-594-128	Sequence 128, App
23	1337	100.0	260	12	US-10-063-553-128	Sequence 128, App
24	1337	100.0	260	12	US-10-063-554-128	Sequence 128, App
25	1337	100.0	260	12	US-10-176-484-378	Sequence 378, App
26	1337	100.0	260	12	US-10-180-550-378	Sequence 378, App
27	1337	100.0	260	12	US-10-183-014-378	Sequence 378, App
28	1337	100.0	260	12	US-10-187-738-378	Sequence 378, App
29	1337	100.0	260	12	US-10-187-740-378	Sequence 378, App
30	1337	100.0	260	12	US-10-187-883-378	Sequence 378, App
31	1337	100.0	260	12	US-10-194-363-378	Sequence 378, App
32	1337	100.0	260	12	US-10-194-460-378	Sequence 378, App
33	1337	100.0	260	12	US-10-194-463-378	Sequence 378, App
34	1337	100.0	260	12	US-10-194-484-378	Sequence 378, App
35	1337	100.0	260	12	US-10-195-884-378	Sequence 378, App
36	1337	100.0	260	12	US-10-195-896-378	Sequence 378, App
37	1337	100.0	260	12	US-10-196-744-378	Sequence 378, App
38	1337	100.0	260	12	US-10-196-755-378	Sequence 378, App
39	1337	100.0	260	12	US-10-196-757-378	Sequence 378, App
40	1337	100.0	260	12	US-10-197-704-378	Sequence 378, App
41	1337	100.0	260	12	US-10-197-710-378	Sequence 378, App
42	1337	100.0	260	12	US-10-198-758-378	Sequence 378, App
43	1337	100.0	260	12	US-10-198-766-378	Sequence 378, App
44	1337	100.0	260	12	US-10-199-304-378	Sequence 378, App
45	1337	100.0	260	12	US-10-199-309-378	Sequence 378, App

ALIGNMENTS

RESULT 1

US-09-796-089-1
; Sequence 1, Application US/09796089
; Patent No. US20020010946A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 21612, 21615, 21620, 21676, 33756, No. US20020010946A1e1
; TITLE OF INVENTION: Human Alcohol Dehydrogenases
; FILE REFERENCE: 35800/208222
; CURRENT APPLICATION NUMBER: US/09/796,089
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/33873
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 09/464,039
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-089-1

Query Match	100.0%	Score 1337;	DB 9;	Length 260;
Best Local Similarity	100.0%	Pred. No. 6	6e-132;	
Matches 260;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVGVCARTVGNIEELAAECKSAGY	60	
Db	1	MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVGVCARTVGNIEELAAECKSAGY	60	
Qy	61	PTGLIPYRCDLSNEEDILSMFSAIRSHSGVDICINNAGLARPDILLSGSTSGKDMFNV	120	
Db	61	PTGLIPYRCDLSNEEDILSMFSAIRSHSGVDICINNAGLARPDILLSGSTSGKDMFNV	120	
Qy	121	NVLALSICTREAYQSMKERNVDDGHHININSMGHRVLPVSVTHFYSATKYAVTALTEGL	180	
Db	121	NVLALSICTREAYQSMKERNVDDGHHININSMGHRVLPVSVTHFYSATKYAVTALTEGL	180	

Qy 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Qy 241 STPAHIQIGDIQMRPTEQVT 260
 Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 2

US-10-206-915-378
 ; Sequence 378, Application US/10206915
 ; Publication No. US20040029221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C513
 ; CURRENT APPLICATION NUMBER: US/10/206,915
 ; CURRENT FILING DATE: 2002-07-26
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 378
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-206-915-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MARGPMEWRDRALALVTGASGGIGAAVARALVQOGLKVVGCAVTGNIIEELAAECKSAGY 60
 Qy 61 PGTLLIPRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
 Db 61 PGTLLIPRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
 Qy 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

Db 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180
 Qy 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Qy 241 STPAHIQIGDIQMRPTEQVT 260
 Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 3

US-10-199-670-378
 ; Sequence 378, Application US/10199670
 ; Publication No. US20040033560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C401
 ; CURRENT APPLICATION NUMBER: US/10/199,670
 ; CURRENT FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 378
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-199-670-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MARGPMEWRDRALALVTGASGGIGAAVARALVQOGLKVVGCAVTGNIIEELAAECKSAGY 60
 Db 1 MARGPMEWRDRALALVTGASGGIGAAVARALVQOGLKVVGCAVTGNIIEELAAECKSAGY 60
 Qy 61 PGTLLIPRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
 Db 61 PGTLLIPRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
 Qy 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYFSATKYAVTALTEGL 180
Qy 181 RQELREQAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 RQELREQAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Qy 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 4

US-10-201-858-378
; Sequence 378, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 378
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARPGMERWRDLALVTGASGGIGAARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
Qy 61 PGTLPYRCDLNSNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTLLSGSTSGKDMFNV 120
Db 61 PGTLPYRCDLNSNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTLLSGSTSGKDMFNV 120

Qy 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYFSATKYAVTALTEGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYFSATKYAVTALTEGL 180
Qy 181 RQELREQAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 RQELREQAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Qy 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 5

US-10-205-890-378
; Sequence 378, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 378
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARPGMERWRDLALVTGASGGIGAARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
Qy 61 PGTLPYRCDLNSNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTLLSGSTSGKDMFNV 120
Db 61 PGTLPYRCDLNSNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTLLSGSTSGKDMFNV 120

Qy 121 NVLALSICTRAYOSMKERNVDDGHHIININSMGHRVLPISVTHFYSAKYAVTALTEGL 180
 Db 121 NVLALSICTRAYOSMKERNVDDGHHIININSMGHRVLPISVTHFYSAKYAVTALTEGL 180
 Qy 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Qy 241 STPAHIQIGDIQMRPTEQVT 260
 Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 6

US-10-208-024-378
 ; Sequence 378, Application US/10208024
 ; Publication No. US20040048335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C538
 ; CURRENT APPLICATION NUMBER: US/10/208,024
 ; CURRENT FILING DATE: 2002-07-29
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 378
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-208-024-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNTEELAAECKSAGY 60
 Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNTEELAAECKSAGY 60
 Qy 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120

Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
 Qy 121 NVLALSICTRAYOSMKERNVDDGHHIININSMGHRVLPISVTHFYSAKYAVTALTEGL 180
 Db 121 NVLALSICTRAYOSMKERNVDDGHHIININSMGHRVLPISVTHFYSAKYAVTALTEGL 180
 Qy 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Qy 241 STPAHIQIGDIQMRPTEQVT 260
 Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 7

US-10-201-853-378
 ; Sequence 378, Application US/10201853
 ; Publication No. US20040053358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C465
 ; CURRENT APPLICATION NUMBER: US/10/201,853
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 378
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-201-853-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNTEELAAECKSAGY 60
 Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNTEELAAECKSAGY 60
 Qy 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120

Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLSSGTSQKDMFNV 120
QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTGL 180
Db 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 8

US-10-063-745-128
; Sequence 128, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLSSGTSQKDMFNV 120
Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLSSGTSQKDMFNV 120
QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTGL 180
Db 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 9

US-10-063-512-128
; Sequence 128, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLSSGTSQKDMFNV 120
Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLSSGTSQKDMFNV 120
QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTGL 180
Db 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 10

US-10-063-513-128
; Sequence 128, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
 DB 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60

QY 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
 DB 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120

QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180
 DB 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

QY 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 DB 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240

QY 241 STPAHIQIGDIQMRPTEQVT 260
 DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 11
 US-10-063-515-128
 ; Sequence 128, Application US/10063515
 ; Publication No. US20030018173A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,515
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 128
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-515-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
 DB 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60

QY 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
 DB 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120

QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180
 DB 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

QY 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 DB 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240

QY 241 STPAHIQIGDIQMRPTEQVT 260
 DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 12
 US-10-063-549-128
 ; Sequence 128, Application US/10063549
 ; Publication No. US20030027986A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,549
 ; CURRENT FILING DATE: 2002-05-02
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 128
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-549-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
 DB 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60

QY 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
 DB 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120

QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180
 DB 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

QY 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 DB 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240

QY 241 STPAHIQIGDIQMRPTEQVT 260
 DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 13
 US-10-063-569-128
 ; Sequence 128, Application US/10063569
 ; Publication No. US20030018168A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,569
 ; CURRENT FILING DATE: 2002-05-02
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 128
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-569-128

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; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-569-128

Query Match      100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
Db 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
QY 61 PGTLLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
Db 61 PGTLLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYATKAVTALTTEGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYATKAVTALTTEGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 14
US-10-063-551-128
; Sequence 128, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvarcoff, Ellen
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; Current Filing Date: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-128

Query Match      100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
Db 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
QY 61 PGTLLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
Db 61 PGTLLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYATKAVTALTTEGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYATKAVTALTTEGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 15
US-10-174-581-378
; Sequence 378, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; Current Filing Date: 2002-06-18
; Prior Application Number: 10/052586
; Prior Filing Date: 2002-01-15
; Prior Application Number: 60/059263
; Prior Filing Date: 1997-09-18
; Prior Application Number: 60/059266
; Prior Filing Date: 1997-09-18
; Prior Application Number: 60/062250
; Prior Filing Date: 1997-10-17
; Prior Application Number: 60/063120
; Prior Filing Date: 1997-10-24
; Prior Application Number: 60/063121
; Prior Filing Date: 1997-10-24
; Prior Application Number: 60/063486
; Prior Filing Date: 1997-10-21
; Prior Application Number: 60/063540
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063541
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063544
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063564
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/063734
; Prior Filing Date: 1997-10-29
; Prior Application Number: 60/063870
; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/064103
; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/065311
; Prior Filing Date: 1997-11-13
; Prior Application Number: 60/066120
; Prior Filing Date: 1997-11-21
; Prior Application Number: 60/066466
; Prior Filing Date: 1997-11-24
; Prior Application Number: 60/066772
; Prior Filing Date: 1997-11-24
; Prior Application Number: 60/069335
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Best Local Similarity	100.0%;	Pred. No. 6.6e-132;			
Matches 260;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MARPGEWRDRDLALVTGASGGICAAVARALVQOGLKVGCARTVGNIEELAAECKSAGY	60		
Db	1	MARPGEWRDRDLALVTGASGGICAAVARALVQOGLKVGCARTVGNIEELAAECKSAGY	60		
Qy	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSQGYDICIINAGLARPDTLISGTSQWKDMFNV	120		
Db	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSQGYDICIINAGLARPDTLISGTSQWKDMFNV	120		
Qy	121	NVLALSCTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSATKYAVNTALTEGL	180		
Db	121	NVLALSCTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSATKYAVNTALTEGL	180		
Qy	181	RQELREAQTHIRATCISPGVVETQFAFLHKDQPEKAAATYEQMKCLKPEDVAEAVLYVL	240		
Db	181	RQELREAQTHIRATCISPGVVETQFAFLHKDQPEKAAATYEQMKCLKPEDVAEAVLYVL	240		
Qy	241	STPAHIQIGDIQMRPTEQVT	260		
Db	241	STPAHIQIGDIQMRPTEQVT	260		

Search completed: September 15, 2004, 11:30:57
Job time : 53 secs

Black

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 11:20:22 ; Search time 40 Seconds
(without alignments)
625.245 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMERWRDLALVTGAS.....STPAHIQIGDIQMRPTEQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	27.5	257	2	AB1866
2	355.5	26.6	273	2	D81878
3	353.5	26.4	273	2	H81140
4	351	26.3	231	2	G90050
5	349.5	26.1	240	2	D95420
6	348.5	26.1	255	2	T44991
7	334.5	25.0	244	2	AH2073
8	332	24.8	249	2	E95283
9	331.5	24.8	240	2	A12681
10	331.5	24.8	248	2	A10678
11	331.5	24.8	271	2	G97463
12	329.5	24.6	248	2	F64908
13	328.5	24.6	248	2	D90897
14	328.5	24.6	248	2	C85720
15	326.5	24.4	253	2	A95223
16	325.5	24.3	240	2	B99667
17	325.5	24.3	240	2	F85517
18	325.5	24.3	260	2	G84171
19	323.5	24.2	244	2	S76993
20	317.5	23.7	252	2	H64122
21	315.5	23.6	253	2	C98087
22	314.5	23.5	238	1	D69930
23	301.5	22.6	250	2	B71859
24	299	22.4	239	2	G82383
25	298	22.3	250	2	B86817
26	296	22.1	231	2	JC7768
27	295	22.1	251	2	G70743
28	293.5	22.0	250	2	E64564
29	293	21.9	267	2	S57593

30 290.5 21.7 260 2 T36118
31 288 21.5 255 2 AF2466
32 278.5 20.8 249 2 JC7857
33 278 20.8 248 2 T44932
34 278 20.8 259 2 A69965
35 276 20.6 255 2 D70635
36 275.5 20.6 249 2 AH3061
37 275.5 20.6 249 2 G98224
38 274.5 20.5 245 2 AG3436
39 274.5 20.5 307 2 E70082
40 273 20.4 233 2 T35242
41 271.5 20.3 246 2 A69621
42 270 20.2 247 2 F92643
43 270 20.2 259 2 AD3082
44 270 20.2 259 2 D98204
45 269 20.1 246 2 H72219

ALIGNMENTS

RESULT 1

AB1866

hypothetical protein all0475 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AB1866

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB1866

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-257 <KUR>

A:Cross-references: GB:BA000019; PIDN:BAB72433.1; PID:gl7129820; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all0475

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 27.5%; Score 368; DB 2; Length 257;

Best Local Similarity 34.0%; Pred.No.3.le-24;

Matches 86; Conservative 53; Mismatches 104; Indels 10; Gaps 6;

Qy 10 RDLALVTGASGGIGAAVARALVQGLKVVGCARTVGNIEELAEK-KSAGYPGTLIYR 68

Db 5 KQIVLITGASSGIGNACARIFAGAGAKLILAAARLAPLQQLADELNQDFGVEIHLL--Q 62

Qy 69 CDLSNEEDILSMFSAIRSOHSQSGVDICINAGLARP-DTLTSGSTSGWKDMFNVLALSI 127

Db 63 LDVRDRPSVESAIASLPAPASDAIDILINNAGLSRGLKHEGDIQDWEEMIDTNVKGILY 122

Qy 128 CTRAYOSMKERNVDDGHIININMSCHRVLPUSVTHFYSAIKYAVTALTEGLRQETREA 187

Db 123 LTRYVVPGMNRG--RGHVNLGSIAGHTYPPG--NVYCGTKAAVKAISEGLKQDL--L 176

Qy 188 QTHTRATCISPGVVETQFAFKLHDKDPEKAAATVEQMKLKPEDVAEAVLYVLSTPAHIQ 247

Db 177 GTPVRVTSVDPGMVETEFSEVRFHGDTERRAKVYQGVNPLTTPEDVADVIFFCATRSRPHV 236

Qy 248 IGDQMRPTEQVT 260

Db 237 INEVILMPVDAQS 249

RESULT 2

D81878

probable oxidoreductase NMA1120 [imported] - Neisseria meningitidis (strain Z3491 serogr C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

Db	59	ESVENALNGIPDFBSIDICLNNAGLGLDTDADKADFEDWETMIQTNVLGLFTLRKIL	118
Qy	134	QSMKERNVDGHIININSMGHRVLPUSVTHFYSAKYAVALTGELQELRBAQTHIRA	193
Db	119	PQWVERG--GGYYMNLGSIAGN--YAYAGSNVYGATKAFVRQFSLNRAEL--ADKNIRV	172
Qy	194	TCISPGVV-ETQAFKLHDKDPEKAAATYEQMKLXPEDVABAVIYVLSTPAHIQIGDIQ	252
Db	173	TNIEPLGCGNTFSNVRFKGDDRAAGVYEGVEFIRPEDIAETALMLDYORPAHMVNVTIE	232
Qy	253	MRPTEQ	258
Db	233	IMPVAQ	238

```

RESULT 4
G90050
hypothetical protein SA2266 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G90050
R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekim
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90050
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <KUR>
A:Cross-references: GB:BA000018; PID:gl3702428; PIDN:BA843569.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homolog
Query Match 26.3% Score 351; DB 2; Length 231;

```

	Matches	83;	Conservative	46;	Mismatches	94;	Indels	20;	Gaps	6
Qy	11	DLRALVTGSGGGIGAAVARALVQQGLKVGVCARTVGNIEELAAECKSAGYPGTLPYRCD	70							
Dd	6	KDIAVVTGAGSGIGEALATLLHEEGAKVVLAGRKKDKLQNVANQLAQDSV--KVVP--TD	61							
Qy	71	LSNEEDILNFSAIRSOHSGVDICINNAGLARPDPTLLSGSTSGWKDMFNVNVALSICTR	130							
Dd	62	VTNKEEVDEMLKIAQQTFGGLDIVNSAGOMLSKITDYQVDENWSDMIDNIKGTLTVAQ	121							
Qy	131	EAYQSMEKNVDDQHIIININSMGHRVLPUSLVTHFYSATKYAVTALTEGRLQEALRAQTH	190							
Dd	122	AALPTMLEQS--SGHLINIASISGFVTKSST--IYSATKAAVHTITQGLEKEL--AKTG	175							
Qy	191	IRATCISPGVVETQPAFKLDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGD	250							
Dd	176	VKVTSISPGVMVDTAITAAYNPSPDRKK-----LDPQDIAEAIVLYALTQPKHVNVE	225							
Qy	251	IQRMP	255							
Dd	226	ITVRP	230							

R54201 5
 Probable oxidoreductase SM2343 [imported] - Sinorhizobium meliloti (strain 102)
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: D95420
 R:Barnett, S.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler,
 J.; Kallman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.;
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium

A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: D95420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <KUR>
A:Cross-references: GB:AR006469; PIDN:AAK65926.1; PID:g14524440; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSYMA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vocholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMA2343
A:Genome: plasmid
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.1%; Score 349.5; DB 2; Length 240;
Best Local Similarity 34.1%; Pred. No. 1.1e-22;
Matches 86; Conservative 47; Mismatches 96; Indels 23; Gaps 6;

Qy 11 DLALVTGASGGIGAARALVQOGLKVVGCAITVGNIEELAAECKSAGYPTLIPYRCD 70
Db 2 DKVILITGASGGIGEGARELGAGAKILLGARQARIEATIRDAG--GTALQAVLD 59
Qy 71 LSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNV-----LA 124
Db 60 VTDHRSAVAAFAQAADVTGWRIDVLVNNAGVMPLESLAAVKVDENRMDVNIKGVWIG 119
Qy 125 LSICTRAYQSMKERNVDDGHHININSMGHRVPLSVTHFYSAKYAVTALTSGLRQEL 184
Db 120 AVLPEMAQRS-----GQIINIGSIGALSVVPTAAV--YCATKFAVRAISDGLRQE- 168
Qy 185 REAOTHIRATCISPGVWETQAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIVLSTPA 244
Db 169 ---STNRVTCVNGVSESLAGTITHEETWAAMDYTRAI--ALOPADIARAVRVIEAPQ 224
Qy 245 HIQIGDIQMRPT 256
Db 225 SVDTEITIRT 236

RESULT 6
T44991
oxidoreductase [imported] - Haloferax volcanii megaplasmid pHV3
C:Species: Haloferax volcanii
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
C:Accession: T44991
R:Farahani, R.; Imbeault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, G.; Charlebois, R.L. submitted to the EMBL Data Library, March 1997
A:Description: Hereditary instability of the megaplasmid pHV3, and filamentation in the
A:Reference number: 222886
A:Accession: T44991
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-255 <FAR>
A:Cross-references: EMBL:U953175; PIDN:AAB71809.1
A:Experimental source: strain D52
C:Genetics:
A:Map position: megaplasmid pHV3
A:Genome: plasmid
A:Note: expressed during heat shock
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.1%; Score 348.5; DB 2; Length 255;
Best Local Similarity 32.9%; Pred. No. 1.5e-22;
Matches 82; Conservative 56; Mismatches 102; Indels 9; Gaps 6;

Qy 12 RLALVTGASGGIGAARALVQOGLKVVGCAITVGNIEELAAECKSAGYPTLIPYRCDL 71

Db 13 KVAIVTGASSGIGSATAKSLASRGASVVVAARRGEELAAATIEDDGGDALVP--TDV 70
Qy 72 SNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNVNLAISICTRE 131
Db 71 TVDDIDALVEATLDEGRIDILVNNAGLMLAIGHADRETLQTITDVNLTLGLITLTHA 130
Qy 132 AYQSMKERNVDDGHHININSMGHRVPLSVTHFYSAKYAVTALTTEGLRQELREAQTHI 191
Db 131 VVPTMMEQ--ESGHVNLSSVVG-RFLQANSSH-YNAAKAGVKMFSDSLRDLVAEAGHV 186
Qy 192 RATCISPGVWETQAFKLHDKDPEKAAATY-EQMKLKPEDVAEAVIVLSTPAHIQIGD 250
Db 187 --SSIEGAVDTLHDIHPDEEVQKNVDYVGTMDALAPEDIARTIIFVVTQPERVDINE 244
Qy 251 IQMRPTQV 259
Db 245 VLIRPLDQV 253

RESULT 7
AH2073
oxidoreductase alr2142 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AH2073
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2073
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-244 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAE73841.1; PID:g17131233; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2142
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.0%; Score 334.5; DB 2; Length 244;
Best Local Similarity 34.4%; Pred. No. 2.3e-21;
Matches 87; Conservative 47; Mismatches 102; Indels 17; Gaps 8;

Qy 11 DLALVTGASGGIGAARALVQOGLKVVGCAITVGNIEELAAECKSAGYPTLIPYR-C 69
Db 6 NKVIAITGASGGIGEAARLARQLRVLGARTDRLEALAAEIRSKGGEA---EYRTL 62
Qy 70 DLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNVNLAISICT 129
Db 63 DVTNLEDMQAFVEPAQDFGLDVVVNNAGLMPLSRLSLRLEKIDENRMDVNIIRGLVHGI 122
Qy 130 REAYQSMKERNVDDGHHININSMGHRVPLSVTHFYSAKYAVTALTTEGLRQELREAQ 189
Db 123 AALPLFKQOR--SGQFVNLSSIGGHNVPYPAV--YCATKFAVWISSEGLRQE-----ST 174
Qy 190 HIRATCISPGVWETQAFKLHDKDPEKAAATYEQMK-CLKPED-VABAVIVLSTPAHIQ 247
Db 175 DIRVTVISPGVTETELASTITDAE--AAEWVEGFRAVIPADAIARAIAPAEICPVEVD 231
Qy 248 IGIQMRPTQV 260
Db 232 VNEIIVRPIGQMS 244

RESULT 8
E95283
probable [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSYMA
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: E95283


```
RESULT 11
G97463
Probable oxidoreductase (AE005204) [imported] - Agrobacterium tumefaciens (strain C58, C
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: G97463
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97463
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86664.1; PID:g15155846; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C 1567
A:Map position: circular chromosome
A:Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology

Query Match      24.8%; Score 331.5; DB 2; Length 271;
Best Local Similarity 32.5%; Pred. No. 4.7e-21;
Matches      80; Conservative 47; Mismatches 108; Indels 11; Gaps 5;

QY 11 DRLALVTGASGGIGAARALVQOGLKVGCARTVGNIEELAAECKSAGYPTGLIPYRCD 70
Db 35 NKVVLTITGASSGIGIARELAGAKLVLGARRMDRLQSLAEELRRKG--AEVVIHTLD 92

QY 71 LSNEDILSMFSAIRSQHSQVDICINNAGLARPDITLLSGSTSGWKDMFNVNVALSICTR 130
Db 93 VTRQSVFAEAGKALQGDIVVNNAGIMPLMSLSLKVDWDRMIEVWKGLVYGYA 152

QY 131 EAYQSMKERNVDDGHIININSMGHRVPLSVTFHYSATKYAVTALTGLRQELREAQTH 190
Db 153 AVLPEMTAR--ASGHIINIASIGALAVSPTRA--YCATKFAVRAISDGLQENED---- 204

QY 191 IRATCISPGVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIVLSTPAHIQIGD 250
Db 205 LRVTCHIFGVVESELAHTITDPAAELMQSYRAI--ALKPDAIGRAVRYAIEQPDVDVNE 263

QY 251 IQMRPT 256
Db 264 IVIRPT 269

RESULT 12
F64908
Probable dehydrogenase (BC 1.1.1.1-) ydfG - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: F64908
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F64908
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-248 <BIAT>
A:Cross-references: GB:AE000251; GB:U00096; NID:g1787814; PIDN:AACT4612.1; PID:g1787820;
A:Experimental source: strain K-12, substrain MGI655
C:Genetics:
A:Gene: ydfG
A:Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:1-178/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match      24.6%; Score 329.5; DB 2; Length 248;
Best Local Similarity 35.9%; Pred. No. 6.2e-21;

F64908
Probable oxidoreductase ydfG [imported] - Escherichia coli (strain O157:H7, substrain EDI
C:Species: Escherichia coli
```

```
Matches      89; Conservative 34; Mismatches 112; Indels 13; Gaps 6;

QY 13 LALVTGASGGIGAARALVQOGLKVGCARTVGNIEELAAECKSAGYPTGLIPYRCDLS 72
Db 2 IVLVGTATAGFECITRRFIQGGHKVIATGRQRERLQELKDELGNLYIAQL-----DVR 56

QY 73 NEEDILSMFSAIRSQHSQVDICINNAGLA-RPDTLLSGSTSGWKDMFNVNVALSICTRE 131
Db 57 NRAAIEELASLPAEWCNIDILVNNAGLALGMEPAHKASVEDWETMTIDTNKGLVYMTRA 116

QY 132 AYQSMKERNVDDGHIININSMGHRVPLSVTFHYSATKYAVTALTGLRQELREAQTHI 191
Db 117 VLPGMVERN--HGHIINIGSTAGS--WPYAGNVYATKAFVRQFSNLNRTDLH--GTAV 170

QY 192 RATCISPGVV-ETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIVLSTPAHIQIGD 250
Db 171 RVTDIEPLGVGTGTEFSNVRFGKDGDKAEKTYQNTVALTPEDVSEAVVWVSTLPAHVNT 230

QY 251 IQMRPTEQ 258
Db 231 LEMMPVTQ 238

RESULT 13
D90897
Probable oxidoreductase ECs2148 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: D90897
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyana, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90897
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <HAY>
A:Cross-references: GB:BA000007; PIDN:BAE35571.1; PID:g13361614; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs2148
C:Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology

Query Match      24.6%; Score 328.5; DB 2; Length 248;
Best Local Similarity 35.9%; Pred. No. 7.6e-21;
Matches      89; Conservative 34; Mismatches 112; Indels 13; Gaps 6;

QY 13 LALVTGASGGIGAARALVQOGLKVGCARTVGNIEELAAECKSAGYPTGLIPYRCDLS 72
Db 2 IVLVGTATAGFECITRRFIQGGHKVIATGRQRERLQELKDELGNLYIAQL-----DVR 56

QY 73 NEEDILSMFSAIRSQHSQVDICINNAGLA-RPDTLLSGSTSGWKDMFNVNVALSICTRE 131
Db 57 NRAAIEELASLPAEWCNIDILVNNAGLALGMEPAHKASIEDWETMTIDTNKGLVYMTRA 116

QY 132 AYQSMKERNVDDGHIININSMGHRVPLSVTFHYSATKYAVTALTGLRQELREAQTHI 191
Db 117 VLPGMVERN--HGHIINIGSTAGS--WPYAGNVYATKAFVRQFSNLNRTDLH--GTAV 170

QY 192 RATCISPGVV-ETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIVLSTPAHIQIGD 250
Db 171 RVTDIEPLGVGTGTEFSNVRFGKDGDKAEKTYQNTVALTPEDVSEAVVWVSTLPAHVNT 230

QY 251 IQMRPTEQ 258
Db 231 LEMMPVTQ 238

RESULT 14
C85720
Probable oxidoreductase ydfG [imported] - Escherichia coli (strain O157:H7, substrain EDI
C:Species: Escherichia coli
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 11:24:07 ; Search time 32 Seconds
(without alignments)
419.461 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPCMERWRDLALVTGAS.....STPAHIQIGDIQMRPTEQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337.5	25.2	249	4	US-09-543-681A-4882
2	331	24.8	249	4	US-09-134-000C-5219
3	317	23.7	265	4	US-09-328-352-6325
4	316.5	23.7	231	4	US-09-134-001C-4397
5	308.5	23.1	272	4	US-09-489-039A-13748
6	308	23.0	248	3	US-09-385-028-11
7	308	23.0	248	4	US-09-726-614-11
8	308	23.0	248	4	US-09-385-040-11
9	307	23.0	256	4	US-09-107-532A-4541
10	269	20.1	288	4	US-09-328-352-6485
11	262.5	19.6	262	4	US-09-328-352-4761
12	232.5	18.9	632	4	US-09-252-991A-23096
13	252	18.8	262	4	US-09-134-000C-4224
14	252	18.8	294	4	US-09-328-352-4992
15	251.5	18.8	256	4	US-09-252-991A-30474
16	250	18.7	742	4	US-09-252-991A-24489
17	249	18.6	266	4	US-09-489-039A-12759
18	247.5	18.5	315	3	US-08-793-035-9
19	247.5	18.5	315	3	US-08-793-035-10
20	239.5	17.9	333	1	US-08-440-856A-4
21	239	17.9	278	4	US-09-489-039A-7309
22	239	17.9	300	4	US-09-976-594-7
23	237.5	17.8	301	4	US-09-252-991A-24032
24	237.5	17.8	337	1	US-08-440-856A-3
25	236.5	17.7	244	1	US-08-762-129-4
26	234.5	17.5	244	1	US-08-762-129-3
27	233.5	17.5	300	4	US-09-907-794A-159

28 233.5 17.5 300 4 US-09-866-028-37 Sequence 37, Appl
29 233.5 17.5 300 4 US-09-905-125A-159 Sequence 159, App
30 233.5 17.5 300 4 US-09-902-775A-159 Sequence 159, App
31 233.5 17.5 301 4 US-09-288-143-98 Sequence 98, Appl
32 232.5 17.4 292 4 US-09-489-039A-12880 Sequence 12880, A
33 232 17.4 246 4 US-08-178-257-9 Sequence 9, Appl
34 232 17.4 279 4 US-09-540-236-3794 Sequence 3794, Ap
35 231 17.3 265 4 US-09-543-681A-7082 Sequence 7082, Ap
36 230.5 17.2 244 2 US-09-090-567-2 Sequence 2, Appl
37 227.5 17.0 246 3 US-09-238-481-2 Sequence 2, Appl
38 227.5 17.0 246 4 US-09-572-810A-2 Sequence 2, Appl
39 226.5 16.9 262 4 US-09-489-039A-11983 Sequence 11983, A
40 225 16.8 254 4 US-09-543-681A-7648 Sequence 7648, Ap
41 224 16.8 250 4 US-09-489-039A-9604 Sequence 9604, Ap
42 223 16.7 203 4 US-09-634-955B-20 Sequence 20, Appl
43 223 16.7 203 4 US-09-634-955B-26 Sequence 26, Appl
44 222.5 16.6 259 4 US-09-252-991A-28945 Sequence 28945, A
45 221.5 16.6 246 4 US-08-178-257-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-543-681A-4882

; Sequence 4882, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543.681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 4882

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-4882

Query Match 25.2%; Score 337.5; DB 4; Length 249;

Best Local Similarity 35.2%; Pred. No. 1.1e-29;

Matches 88; Conservative 39; Mismatches 106; Indels 17; Gaps 7;

QY 13 LALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGYPGTILPVRCDLS 72

Db 2 IIFITGASAGFEAIAHFIHNGHKVIGTARLDKQLQALHOELGDLFY-----PLQDVT 56

QY 73 NEEDILMFSAIRSQHSQGVDCINNAGLA---RPDTLLSGSTSGWKDMFNVNVLALSICT 129

Db 57 DKAVSEIYHQLPQWRSDVLINNAGLGLRP--VDKANLDDWDITMETNKGVLHVT 114

QY 130 REAYQSKERNVDGHIININSMGHRVLPUSVTHFYSATKYAVTALTEGRLQELREAQT 189

Db 115 RALLPSMVERNV--GHINISSTAAS--WPTYMGNNVYGATKAFYKQFSLGLRADLQGGK- 169

QY 190 HIRATCISPGVV-ETQFAFKLHDKPEKAAATYBQMKLPEDVAEAVIYVLSPTAHQI 248

Db 170 -IRVTDIEPLGVGGTEFSLRPFKGTDKVEQTYACADALTPEDVAQVFWTATLPAHVNI 228

QY 249 GDIQMRPTEQ 258

Db 229 NTLMPVPVQ 238

RESULT 2

US-09-134-000C-5219

; Sequence 5219, Application US/09134000C

; Patent No. 6617156

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5219
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5219

Query Match 24.8%; Score 331; DB 4; Length 249;
Best Local Similarity 31.9%; Pred. No. 6.1e-29;
Matches 82; Conservative 54; Mismatches 103; Indels 18; Gaps 7;
QY 6 MERWRDLALVTGASGGIGAARALVQOGLKVVCARTVGNIEELAAECKSAGYPTGLI 65
DB 5 MKSLEKIVIVGSSGIGETARLLARKAKLVIAARRQERLIAIKKELPEA-----TIL 60
QY 66 PYRCDLSNEEDILSMFSAIRSHQSGVDICINNAGLARPDTLLSGSTSGWKDMFNVLAL 125
DB 61 VQADVTKEEVQVRVILKTMEXYGRIDVLFNNAGVWPTAPLIEAPKGEWRQMLDINIMGV 120
QY 126 SICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTEGLRQBLR 185
DB 121 LINGIAAALPIMVEQK--SQIILATDSVAGHVVPDSAV--YCGTKFAVRAIMEGLRQBLR 176
QY 186 EAQTHIRATCISPGVETQFAFKLHDKDPEKAAAT---YEQMKC-LKPEDVAEAVIYVLS 241
DB 177 E--NNIKTIISPGAVQTE----LYQTISNRVVAETLHLEQSLWGLKAEDIAQAVYFAID 230
QY 242 TPAHQIGDIOMRPTEQ 258
DB 231 TPDMSISEMVRPTIQ 247

RESULT 3
US-09-328-352-6325
; Sequence 6325, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6325
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6325

Query Match 23.7%; Score 317; DB 4; Length 265;
Best Local Similarity 34.7%; Pred. No. 2.5e-27;
Matches 87; Conservative 41; Mismatches 107; Indels 16; Gaps 8;
QY 13 LALVTGASGGIGAARALVQOGLKVVCARTVGNIEELAAECKSAGYPTGLIYPRCDLS 72
DB 15 LALVTGASAGFGYSISKSIGYKVGCGRAEKLEBLQKLGNFYPLVF-----DMT 69
QY 73 N-EEDILSMFSAIRS--QHSQVDICINNAGLARP--DTLLSGSTSGWKDMFNVLALSLIC 128
DB 70 DTAENINKLFELPNEFQIDQIDLLVNNAGLALGHEPADKADLDWYTMIDTNVKGITV 129
QY 129 TREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTEGLRQBLREQ 188

DB 130 TRLLPILSMVKKK--SGLIINMGSIAG--TYPYGGNVYGATKAFVEQFSLNLRADL--AG 183
QY 189 THIRATCISPGV--ETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSPTAHQ 247
DB 184 TGVVRVNIPEGLCGGTESLVRFKGQDEKANSKYDKKNPILPEDTANTVAMIASOPPHIN 243
QY 248 IGDIOMRPTEQ 258
DB 244 INRIEMMETTQ 254

RESULT 4
US-09-134-001C-4397
; Sequence 4397, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4397
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4397

Query Match 23.7%; Score 316.5; DB 4; Length 231;
Best Local Similarity 29.9%; Pred. No. 2.3e-27;
Matches 75; Conservative 56; Mismatches 97; Indels 23; Gaps 7;
QY 6 MERWRDLALVTGASGGIGAARALVQOGLKVVCARTVGNIEELAAECKSAGYPTGLI 65
DB 2 MAKVKERVAVVTGASSGIGEAIANKLSQOGASIVLVGRNEORLEIVQOLANN---PAKV 58
QY 66 PYRCDLSNEEDILSMFSAIRSHQSGVDICINNAGLARPDTLLSGSTSGWKDMFNVL--A 124
DB 59 --TADVTYKSNIDDMKXVIDHFGHIDIVNSAGOSLSKITYNVQMDTWIDVNIKGT 116
QY 125 LSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTEGLRQBL 184
DB 117 LHLVQATLPYLLKQ---SSGHIINLASVSGFE--PTKTNAVYGATKAAIHAITQSLKEL 171
QY 185 REAOTHIRATCISPGVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSPTA 244
DB 172 --ARTGVKVTISPGMVDT-----PMTGTDGFERKKLEAQNIADAVVYALTQPS 219
QY 245 HIQIGDIOMRP 255
DB 220 HNVNVEVTIRP 230

RESULT 5
US-09-489-039A-13748
; Sequence 13748, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13748

[illegible]

Query Match	23.0%;	Score 308;	DB 4;	Length 248;
Best Local Similarity	31.3%;	Pred. No. 2.4e-26;		
Matches	78;	Conservative 50;	Mismatches 111;	Indels 10; Gaps 5
QY	12	RLALVTGSGGICAAVARALVOOGLKWCARTVGNIEELAAECSAGYPGTLPIPYRCDL	71	
				:::
Db	8	KVALITGSSGIGETARALAAEGAAVAIAARRVEKLRALGDELTAAGAKVHVL--ELDV	65	
QY	72	SNEEDILMSFAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVVNLALSICRRE	131	
		::: ::		:::
Db	66	ADROQGVDAAVSTVEALGGDLTLVNAGIMLLGPVEDADTTTWTMRIDTNLLGLMYMTRA	125	
QY	132	AVQSMKERNVDGHIININSMSGHRVLPUSVTHFYSAKYAVTALTEGRQBLERAQTHI	191	
		::: ::		:::
Db	126	ALPHILR---SKGTVVQMSIAGR--VNVRNAAVQATKFGVNASETLRQEVTE--RGV	178	
QY	192	RATCISPGVVFQFAFKL-HDKDPEKAAATYQMKCLKPEDVAEAVIYVLSTPAHIQID	250	
Db	179	RVVWIEPGTDTDELRGHIHTHTAKMEYEQIRISQIRKLAQDIAEAVRYAVTAPHATVHE	238	

	Query Match	23.0%;	Score 307;	DB 4;	Length 256;
	Best Local Similarity	30.4%;	Pred.No. 3.2e-28;		
	Matches	Conservative 54;	Mismatches 106;	Indels 14;	Gaps 6;
QY	11	DRLALVTGASGGICAAVARALVQOGLKVWGCVARTVGNIIEELAEAFCKSGAGPFTLIPYRCD	70		
Db	17	EKVVIMWGAASSIGEGATTKLLAEGAKLIVAAAREDRALKAKESLPEA----	ELYIQTAD 72		
QY	71	LSNEEDILSMFSFATSRSQHSGVDVICINNAGIARPTDTLLSGSTSGWKDMFNVNVALSICTR	130		
Db	73	VRFDAQOVAIDLAAMEKFGRIDVLVYNNAGMTAPLVGEHRDEWQNQLMDINIMGVLNGIS	132		
QY	131	EAYQSKMERNVDDGHIIININSMSGRHVLPLSVTHFYSATKYAVTALTEGRLQRLEAQTH	190		
Db	133	AVLPIMERQOK--SGHIISTDSVAUGHVVPDPSAV--YCCTKEFAVEPAIMEGLRQEOR--QNN	186		
QY	191	IRATCISPGVNVEOTAFKLIHKDKDEKAANTYEOMK--CLKPEDVAEAVIVLSTPAHQIQI	248		

Db 187 IKSIISGAVQTELYQTISK--KAALHLHAQKEWGLTSEDIASAVAFAPETDRMSV 244
QY 249 GDQWRPTEQ 258
Db 245 SNMIIRPTQ 254

RESULT 10

US-09-328-352-6485
; Sequence 6485, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6485
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6485

Query Match 20.1%; Score 269; DB 4; Length 288;
Best Local Similarity 29.6%; Pred. No. 7.6e-22;
Matches 73; Conservative 50; Mismatches 96; Indels 28; Gaps 7;

QY 6 MERWRDLALVTGASGGIGAARALVQOG-----LKVVGCAATVGNIEELAECKSA 58
Db 5 MKSEFNKVAATGAGSGIGQALALAKQCHLALDISEAGLAKTV-----ELLAP---- 56
QY 59 GYPOTLIPYRCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLTSGSTSGWKDMF 118
Db 57 -YSKVVTQKVDVAKROEVATWAKAVVDEHGQVNLIFENNAGVAIGSTAEGVSYEDLEWLI 115
QY 119 NVNVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYSAKYAVTALTE 178
Db 116 GINFWGVYGTKEFLPYLKQSG--DGHIIINISSMFLGTAQPTQSA--YNASKFAVRGFT 171
QY 179 GLRELREAQTHIRATCISPGVWETQF--APFLHDK-----DPEKAAATVEOMKCLKPE 230
Db 172 SLRQELDMQNAVGTATVHPGGIRTNIAKARMNSVQSLGMDPLKSDQDAFDKLLRTPAD 231
QY 231 DVAEAVI 237
Db 232 DAAQIL 238

RESULT 11

US-09-328-352-4761
; Sequence 4761, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4761
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4761

Query Match 19.6%; Score 262.5; DB 4; Length 262;
Best Local Similarity 30.0%; Pred. No. 3.6e-21;
Matches 72; Conservative 49; Mismatches 108; Indels 11; Gaps 5;

QY 12 RLALVTGASGGIGAARALVQOGLKVVGCARTVGNIEELAECKSAGYPGTLIPYRCDL 71
Db 24 KVALVTGASRGIGAAIAQQLIQDGYFVVGTATSESGAKLT--DSFGEQAGL--ALDV 78
QY 72 SNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLTSGSTSGWKDMFNVNVLALSICTRE 131
Db 79 RNLDEIEAVVSHIQONYGFLVIVNNAGITKDNLLRMSEDDDDILNIHLKAVYRLSKR 138
QY 132 AYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYSAKYAVTALTEGLRQELREAQTHI 191
Db 139 VLKGMTKARF--GRIIINISSVVAHFANPQAN--YSAKAGIEAFSRSLAKEMGSRQ--I 192
QY 192 RATCISPGVWETQFAPFLHDKDPEKAAATVEOMKCLKPEDEVAEAVIYVLSVTHFYSA 251
Db 193 TVNSVAPGFIATMTDALSDIRKMSDQVALNGLGEFQDIANAVSFLASDKAGYITGTV 252
RESULT 12
US-09-252-991A-23096
; Sequence 23096, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23096
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23096

Query Match 18.9%; Score 252.5; DB 4; Length 632;
Best Local Similarity 27.4%; Pred. No. 2e-19;
Matches 74; Conservative 56; Mismatches 109; Indels 31; Gaps 9;

QY 6 MERWRDLALVTGASGGIGAARALVQOGLKVVGCARTVGNIEELAECKSAGY-PGTL 64
Db 342 MKSEFNKVAATGAGSGIGRALAVELGRQCHLADVNAAALBETRQLLASSGVRVSTA 401
QY 65 IPYRCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLTSGSTSGWKDMFNVL 124
Db 402 V---VDVADREQVQAWADKAASEHGRVNLIFNNAGVAHAGTVEGSDYSEYEWNNINFWG 458
QY 125 LSICTREAYQSMKERNVDDGHIININSMGHRVLP-LSVTHFYSAKYAVTALTGLRQE 183
Db 459 VNGTKAFLPHLKASG--NGHVNVSVSVFGLFAQPGMSA---YNATKYAVRGFTESLRQE 513
QY 184 LREAQTHIRATCISPGVWETQFA-----FKLHDKDPEKAAATY-EOMKCLKPEDEV 233
Db 514 LDMEDSGVSASCVHPGGIKTNIAKARMESMAKVITGQAPDKAREQFNQDQLLRTTPEKAA 573
QY 234 EAVI-----YVLSVTHFYSAKYAVTALTGLRQE 254
Db 574 QVILRGVQRDSRRLITGTDHAI--DVMLR 601

RESULT 13

US-09-134-000C-4224
; Sequence 4224, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032

Search completed: September 15, 2004, 11:30:00
Job time : 33 secs

Query Match 18.8%; Score 252; DB 4; Length 294;
Best Local Similarity 28.4%; Pred. No. 6.6e-20;
Matches 75; Conservative 47; Mismatches 106; Indels 36; Gaps 9

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 16:23:41 ; Search time 85 Seconds
(without alignments)
1697.497 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMRWRRLALVTGAS.....STPAHQIGDIQMRPTEQVT 260

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 692709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	350	26.2	1788	4	US-08-956-171E-130
2	337.5	25.2	750	4	US-09-543-681A-710
3	331	24.8	750	4	US-09-134-000C-1814
C 4	326.5	24.4	3149	4	US-08-961-527-31
5	326.5	24.4	6133	4	US-09-453-702B-15
6	322.5	24.1	1830121	4	US-09-557-884-1
7	322.5	24.1	1830121	4	US-09-643-990A-1
8	318	23.8	763	4	US-09-221-017B-723
9	317	23.7	798	4	US-09-328-352-2199
10	316.5	23.7	696	4	US-09-134-001C-1560
11	308.5	23.1	819	4	US-09-489-039A-6577
C 12	308	23.0	744	3	US-09-385-028-22

C 13	308	23.0	744	4	US-09-726-614-22	Sequence 22, Appl
C 14	308	23.0	744	4	US-09-385-040-22	Sequence 22, Appl
C 15	308	23.0	11604	3	US-09-385-028-13	Sequence 13, Appl
C 16	308	23.0	11604	4	US-09-726-614-13	Sequence 13, Appl
C 17	308	23.0	11604	4	US-09-385-040-13	Sequence 13, Appl
C 18	308	23.0	15079	3	US-09-385-028-1	Sequence 1, Appl
C 19	308	23.0	15079	4	US-09-726-614-1	Sequence 1, Appl
C 20	308	23.0	15120	4	US-09-385-040-1	Sequence 1, Appl
C 21	307	23.0	771	4	US-09-107-532A-887	Sequence 887, App
C 22	295	22.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 23	295	22.1	441529	3	US-09-103-840A-1	Sequence 1, Appl
C 24	269	20.1	867	4	US-09-328-352-2359	Sequence 2359, Ap
C 25	262.5	19.6	789	4	US-09-328-352-635	Sequence 635, App
C 26	252.5	18.9	1038	4	US-09-252-991A-6549	Sequence 6549, Ap
C 27	252.5	18.9	1899	4	US-09-252-991A-6525	Sequence 6525, Ap
C 28	252	18.8	789	4	US-09-134-000C-819	Sequence 819, App
C 29	252	18.8	885	4	US-09-328-352-866	Sequence 866, App
C 30	251.5	18.8	771	4	US-09-252-991A-13903	Sequence 13903, A
C 31	251.5	18.8	1995	4	US-09-252-991A-13546	Sequence 13546, A
C 32	250.5	18.7	6977	4	US-08-178-237-8	Sequence 8, Appl
C 33	250	18.7	996	4	US-09-252-991A-7849	Sequence 7849, Ap
C 34	250	18.7	1743	4	US-09-252-991A-7635	Sequence 7635, Ap
C 35	250	18.7	2229	4	US-09-252-991A-7918	Sequence 7918, Ap
C 36	249	18.6	801	4	US-09-489-039A-5588	Sequence 5588, Ap
C 37	249	18.6	31940	4	US-09-596-002-13	Sequence 13, Appl
C 38	247.5	18.5	1155	3	US-08-793-035-1	Sequence 2, Appl
C 39	247.5	18.5	1185	3	US-08-793-035-1	Sequence 1, Appl
C 40	247.5	18.5	1419	4	US-09-252-991A-13796	Sequence 13796, A
C 41	244.5	18.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 42	244.5	18.3	441529	3	US-09-103-840A-1	Sequence 1, Appl
C 43	239.5	17.9	1187	1	US-08-440-856A-2	Sequence 2, Appl
C 44	239	17.9	837	4	US-09-489-039A-138	Sequence 138, App
C 45	239	17.9	1010	4	US-09-976-594-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-08-956-171E-330/c
; Sequence 330, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

QY 209 LeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLysCysLeuLys 228
 Db 565 CGCTTTAAAGGTGATACCAAGTAAAGTAGAACAACTTATGCAGGACCATCGCTTACT 624
 QY 229 ProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGlnIle 248
 Db 625 CCTGAAGATGTTGCACAGCGGTTTTCGACGGCAACATTCCTGCACATGTTAATATT 684
 QY 249 GlyAspIleGlnMetArgProThrGluGln 258
 Db 685 AATACGCTTGAGATGATGCCCGCTCAGTCAA 714

RESULT 3
 US-09-134-000C-1814
 ; Sequence 1814, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1814
 ; LENGTH: 750
 ; TYPE: DNA
 ; ORGANISM: Enterococcus faecalis
 US-09-134-000C-1814

Alignment Scores:
 Pred. No.: 1.52e-33 Length: 750
 Score: 331.00 Matches: 83
 Percent Similarity: 51.33% Conservativity: 52
 Best Local Similarity: 31.56% Mismatches: 98
 Query Match: 24.76% Indels: 30
 DB: 4 Gaps: 7

US-10-063-735-128 (1-260) x US-09-134-000C-1814 (1-750)

QY 6 MetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
 Db 13 ATGAATCATTTATCAGAAAAAGTATTGTTATCATCGGCGCTTCAGTGGCATCGTGAG 72
 QY 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
 Db 73 GCAACAGCCGCTTACTTGCAGAAAAAGGAGCGAAGTTAGTCATTCGACGACGTCGACAA 132
 QY 46 GlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
 Db 133 GAACGTTTAAATGCTTAAAAAAGAACTTCCTGAAGCA-----ACGATTCCTC 180
 QY 66 ProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArg 85
 Db 181 GTGCACACAGCAGATGTAAACAAAGAGAGAGAGTTACGCTGTAATCAACGCTTACAAATG 240
 QY 86 SerGlnHisSerGlyValAlaPileCysIleAsnAlaGlyLeuAlaArgProAspThr 105
 Db 241 GAAAAATATGACCAATGATGTTCTTTTAAACAATGCAGGAGTTATGCCAACGGCGCT 300
 QY 106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeu 125
 Db 301 CTTATTTGAAGCACCACAAAGGAGATGCGCTCAATGCTAGATATTAATATTATGCGGTGT 360
 QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspGlyHis 145
 Db 361 TTAATGCGATTCGGCAGTTCTTCCATTAATGTTGAACAAAA-----TCAGGGCAG 414
 QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165

Db 415 ATTATGCTACTGATCTGTGCAGACATGCTGTTTTATCCAGATTCGGCTGTC----- 468
 QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlnGluArgGlnGluLeuArg 185
 Db 469 TACTGTGGAACAAGTGTCTGCTTCGAGCAATATTATGGAAGGATTGCGACAAAGCAAGA 528
 QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
 Db 529 GAG-----AATAACATTAAATCAACGATTATTTCCAGAGTGTGTACAAACAGAACTT 582
 QY 206 -----AlaPheLysLeuHisAspLysAspProGluLys 216
 Db 583 TATCAACAATTTCTAATCGAGTAGCTGAACGTTACAT----- 624
 QY 217 AlaAlaAlaThrTyrGluGlnMetLysCys-----LeuLysProGluAspValAlaGluAla 235
 Db 625 -----CTAGAACAGTTAAGTTGGGCTTTAAAGGCGGAAGACATTGCGCAAGA 672
 QY 236 ValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgPro 255
 Db 673 GTGGTCTTTGCGATAGACACGCCAGATCGTATGTCATCAGTGAATGTTGTCGCGCG 732
 QY 256 ThrGluGln 258
 Db 733 ACCACACAA 741

RESULT 4

US-08-961-527-31/c
 ; Sequence 31, Application US/08961527
 ; Patent No. 6420135
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 391
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/961,527
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PB340P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3149 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 US-08-961-527-31

Alignment Scores:
 Pred. No.: 6.2e-32 Length: 3149
 Score: 326.50 Matches: 85
 Percent Similarity: 52.36% Conservativity: 48
 Best Local Similarity: 33.46% Mismatches: 100

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Query Match:      24.42%      Indels:      21
DB:               4          Gaps:         5

US-10-063-735-128 (1-260) x US-08-961-527-31 (1-3149)

QY 15 LeuValThrGlyAlaSerGlyGlyLeuGlyAlaValAlaValAlaValGlnGln 34
Db 1331 GTGATTACAGAGGACATCAGGATCGGTGAAGCATTTGGCGGTCTTATCTGGAGCAG 1272
QY 35 GlyLeuValValGlyCysAlaAlaArgThrValGlyAsnIleGluGluLeuAlaGlu 54
Db 1271 GGTGAGGATGCTGTTCTAACAGGACGCGATAGACAGCTTAAAGCGGAG 1212
QY 55 CysLysSerAlaGlyTyrProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGlu 74
Db 1211 TTTGAGAACTTTTCCAAATCAACAGCTTTGACCTTCTCTAGATGTCCAGGATATG 1152
QY 75 GluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCys 94
Db 1151 ACAATGGTAAAGACTGCTGCTCTGATATTTAGAAACGATAGGTACAGTTCATCTG 1092
QY 95 IleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyr 114
Db 1091 GTCATACAGCAGGACTGCTCTT-----GGCTTAGCTCCCTAT 1053
QY 115 LysAsp-----MetPheAsnValAsnValLeuAlaLeuSer 126
Db 1052 CAAGACTATGAGAGTTGGATATGCTGACCATGTTGGATACCAATGTCAAAGGTTTGATG 993
QY 127 IleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHisIle 146
Db 992 CGAGTCATCGCTGTTCTTCCAGCAATGGTAAAGCCAT-----CAAGTCTATTT 939
QY 147 IleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPheTyr 166
Db 938 ATCAATATGGGTCAACCGCAGGA-----ATTATGCTATGCTGGTGCAGCTGTTTAC 885
QY 167 SerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnLeuArgGlu 186
Db 884 TCAGCCACCACAGCGGCGATTTTTCAGATGGACTCGCA-----ATTGATACC 831
QY 187 AlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPheAla 206
Db 830 ATCGCAACGGATATCAAGTGCAGCATTTCAGCTGGAAATGTGCAACACAGATTTTCT 771
QY 207 PheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLysCys 226
Db 770 ACAGTGGCTTTTCATGGTGATAAAGAACGAGCTGCGCTTTACCAAGGAATAGAAGCT 711
QY 227 LeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIle 246
Db 710 TTGCAAGCTCAGGATATTCAGATACAGTAGTCTATGTGACTAGTCAACCTCGTGTGT 651
QY 247 GlnIleGlyAspIleMetArgProThrGluGlnValThr 260
Db 650 CAGATTACAGATATGACCATATGCCCAATCAACAGCGGACCA 609

```

RESULT 5

US-09-453-702B-15
Sequence 15, Application US/09453702B
Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison

```

STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 6133
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-453-702B-15

Alignment Scores:
Pred. No.:      1.85e-31      Length:      6133
Score:          326.50      Matches:      85
Percent Similarity: 50.00%      Conservative: 43
Best Local Similarity: 33.20%      Mismatches: 105
Query Match:      24.42%      Indels:       23
DB:               4          Gaps:         6

US-10-063-735-128 (1-260) x US-09-453-702B-15 (1-6133)

QY 7 GluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAlaLa 26
Db 651 GAGACGCTAATGATAGGTATTAATTAATACCGCGCATCAAGTGTATTGGGAAGT 710
QY 27 ValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGly 46
Db 711 ATTGCCAGAGAGCTTGGAAATGACAGGTGCAAAAGTTTACTGGGAGCACGAGAGTTGAG 770
QY 47 AsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIlePro 66
Db 771 CGTATCGAAGCCATTGCAACACCGAAATCTGCCCGCAGGA-----GGAATTGCTAAAGCG 824
QY 67 TyrArgCysAspLeuSerAsnGluAspIleLeuSerMetPheSerAlaIleArgSer 86
Db 825 CGGGAGTTGGATGTCACAGCCGACAGTCCATGCGCGATTTCGTGCAAGCAGCGCTGGAT 884
QY 87 GlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeu 106
Db 885 AGCTGGGGGAGATTGATGTTCTTATCAATAATGCGGGCGTTATGCGCGCTTTTCACGCTT 944
QY 107 LeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnVal-----122
Db 945 GCAGCAGGAAACCAAGATGATGGCGCTCATTGCTGATATCAAGAGTGTACTG 1004
QY 123 -----LeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 1005 TGGGGAATTGGCGCTGCTACTTCCGGTGTAGTGAAGCACAGGGTTC-----1049
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 1050 -----GGTCAGATAATCAATCTTGTGTTCTTATTTGGTGGCCTTTCTGTTGGCCACA 1100

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QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
 Db 1101 GCGCAGTC-----TATGTGTCATCAAAATTTGCGAGTACGGCTATTTCGATGGCTTA 1154
 QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisLeuArgAlaThrCysIleSerProGlyVal 200
 Db 1155 CGGCAGGAA-----AGTCGAAATCCGTGTGACCTGCGTAAATCCTGGCGTT 1202
 QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
 Db 1203 GTCGAAAGTGAACCTGGCTTCAACCAATTCATCCCATGCGAAACCATGAAGGCAATGACGCC 1262
 QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
 Db 1263 TACCGTTCTGTT--GCACCTTCAACCGCGGATATGCGCGTGTGTGAAGCAATTAAT 1319
 QY 241 SerThrProAlaHisIleGlnIleGlyAspLeuGlnMetArgProThr 256
 Db 1320 GAATCTCCGAAAGCGTTGTATACCAACCGAAATTACCATCAGACCCACT 1367

RESULT 6

US-09-557-884-1
 ; Sequence 1, Application US/09557884
 ; Patent No. 6506581
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleischmann et al.
 ; TITLE OF INVENTION: The Nucleotide sequence of
 ; the Haemophilus influenzae Rd Genome, Fragments
 ; Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3 1/2 inch diskette
 COMPUTER: Dell Pentium
 OPERATING SYSTEM: MS DOS v6.22
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/557,884
 FILING DATE: 25-Apr-2000
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/476,102
 FILING DATE: JUN-5-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Michelle S. Marks
 REGISTRATION NUMBER: 41,971
 REFERENCE/DOCKET NUMBER: PB186P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 183021 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1
 Alignment Scores:
 Pred. No.: 7.17e-27 Length: 183021
 Score: 322.50 Matches: 78
 Percent Similarity: 51.57% Conservative: 53
 Best Local Similarity: 30.71% Mismatches: 110
 Query Match: 24.12% Indels: 13
 DB: 4 Gaps: 6

US-10-063-735-128 (1-260) x US-09-557-884-1 (1-1830121)
 QY 7 GluArgTrrArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAlaAla 26
 Db 1517820 GAAAAAATGAAACACTACTACTGTCATTAGTAACAGGTGCAACCGCAGGCTTTGGCTTGCA 1517879
 QY 27 ValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGly 46
 Db 1517880 ATCTGTAATAAATTCATCGAAGCAGGCTTATAAGTGATTGGCAGGCGAGCTGCAGAT 1517939
 QY 47 AsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIlePro 66
 Db 1517940 CGATTAGCAGAAATCCATTCAATTTGGCAAT-----AATTTTCTACCG 1517984
 QY 67 TyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArgSer 86
 Db 1517985 CTTGCTTTTGACATTCGTGATGAACAAGCCCAATTAACGCTCTAAATACCTTCTCTGAA 1518044
 QY 87 GlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgPro---AspThr 105
 Db 1518045 GCGTGGCAAGCGTCGATTTATTAGTGAATATCAGGTTTAGCTTGGGATTAGAGCG 1518104
 QY 106 LeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeu 125
 Db 1518105 GCACATAAAGCGGATTTACAAGATTGGTATCAGATGATTGATCAACATCAAGGATTG 1518164
 QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
 Db 1518165 GTTACTATCATCGCTTGTGTCCTCAATATGCTGGCTGTAATTAC-----GGCGAG 1518218
 QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
 Db 1518219 ATTAATCAATTGAGTTCAATTGCGAGT-----ACTTATCCTTATGCGAGCAGTAATGTA 1518272
 QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
 Db 1518273 TATGCTGGAACCTAAAGCTTTTGTCACACAATTAGCTTAATTTACGAGCGGATCTG--- 1518329
 QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValVal---GluThrGln 204
 Db 1518330 ---GCAGGCACAAAAATTCGAGTAAGCAATGTTGAACCGGTTTATGTGGCGGTACGGAG 1518386
 QY 205 PheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMet 224
 Db 1518387 TTCTCTAATGTGCGTTTTCACGCGCATGATGAAGAGCGCCAAAGTCTATGAAAACGTG 1518446
 QY 225 LysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAla 244
 Db 1518447 CAATCGGTTGAGCTGAGATATTGGAACATTGTTATTTGGCTTTCATCAACACCTGAA 1518506
 QY 245 HisIleGlnIleGlyAspIleGlnMetArgProThrGluGln 258
 Db 1518507 CAGCTGAACATTAAATCGTATTGAAGTAATGCCAACCGCTCAA 1518548

RESULT 7

US-09-643-990A-1
 ; Sequence 1, Application US/09643990A
 ; Patent No. 6528289
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert D. Fleischmann
 ; Mark D. Adams
 ; Owen White
 ; Hamilton O. Smith
 ; J. Craig Venter
 ; TITLE OF INVENTION: The Nucleotide sequence of
 ; the Haemophilus influenzae Rd Genome, Fragments
 ; Thereof, and Uses Thereof
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville,

STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
Alignment Scores:
Pred. No.: 7,17e-27 Length: 1830121
Score: 322.50 Matches: 78
Percent Similarity: 51.57% Conservative: 53
Best Local Similarity: 30.71% Mismatches: 110
Query Match: 24.12% Gaps: 13
DB: 4
US-10-063-735-128 (1-260) x US-09-643-990A-1 (1-1830121)
Qy 7 GluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyLeuGlyAlaAla 26
Db 1517820 GAAAAATGAAACTACTACTGATAGTAAACAGGTGCAACCGCAGGCTTTGGCTGGCA 1517879
Qy 27 ValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGly 46
Db 1517880 ATCTGTAATAAATGATCGAACGAGCTATAAAGTATTGGCAGCGGACGTCAGAT 1517939
Qy 47 AsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIlePro 66
Db 1517940 CGATTAGCAAGAAATCCATTCAATTTGGCAAT-----AATTTTCTACCG 1517984
Qy 67 TyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArgSer 86
Db 1517985 CTTGGCTTTGACATTCGTGTAAGCAACGCCAATTAACGCTCTAAATACCTTCTCTGAA 1518044
Qy 87 GlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgPro---AspThr 105
Db 1518045 GCGTCGCAAGCGGTGATTTATTAGTAATAATGACAGGTTTAGCTTGGGATTAGAGCG 1518104
Qy 106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeu 125
Db 1518105 GCACATAAGCGGATTTACAGATTGGTATCATGATGATTACCAACATCAAGGATTG 1518164
Qy 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
Db 1518165 GTTACTATCACTCGCTTGTGTGTCAAATATGGTGGCTCGTAATAC-----GGGAG 1518218
Qy 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
Db 1518219 ATTATCAATTTGAGTTCAATTGCAGGT-----ACTTATCCTTATGACGAGCAATAATGTA 1518272
Qy 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
Db 1518273 TATGTTGGAACATAAAGCTTTTGTACACAAATTTAGCTTAAATTTACGAGCGGATCTG--- 1518329
Qy 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValVal---GluThrGln 204
Db 1518330 ---GCAGCACAAAAATTCGAGTAAGCAATGTTGAACCGGTTTATGTGGCGGTACGGAG 1518386
Qy 205 PheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThrTyrGluGlnMet 224
Db 1518387 TTCCTAATGTGCGCTTTTTCACGCGGATGATGAAAGAGCGCAAAAGTCTATGAAAAACGTG 1518446
Qy 225 LysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAla 244
Db 1518447 CAATCGGTTACGCTGAAGATATTGCGAAACATTTGTTATGCTTCATCAACACCTGAA 1518506
Qy 245 HisIleGlnIleGlyAspIleGlnMetArgProThrGluGln 258
Db 1518507 CACGTGAACATTAATCGTATTGAAGTAATGCCAACCGCTCAA 1518548
RESULT 8
US-09-221-017B-723
; Sequence 723, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Rose, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Montoy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; INFORMATION FOR SEQ ID NO: 723:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)

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; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...763
US-09-221-017B-723

```

Alignment Scores:

```

Pred. No.: 7,8e-32 Length: 763
Score: 318.00 Matches: 85
Percent Similarity: 52.48% Conservative: 42
Best Local Similarity: 35.12% Mismatches: 105
Query Match: 23.78% Indels: 10
DBs: 4 Gaps: 7

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US-10-063-735-128 (1-260) x US-09-221-017B-723 (1-763)

```

QY 16 ValThrGlyAlaSerGlyGlyLeuAlaValAlaValAlaValGlnGlnGly 35
DB 3 ATCACCGGAGCACATCCGCATCGGTGCGCTCGCTCGCTCGCTCGCTCGAT 62
QY 36 LeuLysValValGlyCysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCys 55
DB 63 TATAACCTTATCATCACGGGACGCGCTCGGAACGTTTGCAGAAACATTCGCGATGAATC 122
QY 56 LysSerAlaGlyTyrProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGlu 75
DB 123 AGA---GCTGAATACCTTGTGGAATCTCTCCGCTCTCTTTTCGATGTCGCAATCGCAA 179
QY 76 AspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIle 95
DB 180 GAAGTAGAGCCATTTCGGCAATTTCGCTGATCCTTGGCAGCGCTTTCGCTCTCGTG 239
QY 96 AsnAsnAlaGlyLeuAlaArgPro---AspThrLeuLeuSerGlySerThrSerGlyTyr 114
DB 240 AATAATGCGCGTTCGGCAGCGGACTCGACCCCATACAGTCGGTGACATTCGAAGACTGG 299
QY 115 LysAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGln 134
DB 300 GAACGTATGATAGACACCAATATCAAGGACTCTCTACGTAACCTCGCACCAATCAGCCCG 359
QY 135 SerMetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSerMetSerGly 154
DB 360 GGTATGATAGCCGAGCGCC-----GGCATATCATCAATATCGGTCTATTGCCGCG 413
QY 155 HisArgValLeuProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThr 174
DB 414 AAGGAAGTT-----TACTCTAAACGCAATGCTATTTCGTCACGACGATGCCGTAGAT 467
QY 175 AlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThr 194
DB 468 GCTCTTCGAAAGCGATCGGTATAGATATG-----CTTCCTTATGGCATCAAAAGTCACA 521
QY 195 CysIleSerProGlyValValGluThrGlnPheAlaPhe---LysLeuHisAspLysAsp 213
DB 522 CAGATTTCTCCGGAGCAGTGGAGACGAGTTCGCTGGTGGCTTCATGAT---GAT 578
QY 214 ProGluLysAlaAlaAlaThrTyrTyrGluGlnMetLysCysLeuLysProGluAspValAla 233
DB 579 CAGGCCAAGGCGGATCGCGGTACAAAGGCTTCCTCTCTCTGTGCGAAGACATAGCG 638
QY 234 GluAlaValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMet 253
DB 639 GAGTGTATGCGGCGTACTGAACCTGCTGATAATATCTGTATCAACGATATGCTGTC 698
QY 254 ArgPro 255
DB 699 ATGCCG 704

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RESULT 9

US-09-328-352-2199

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; Sequence 2199, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2199
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2199

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Alignment Scores:

```

Pred. No.: 1,14e-31 Length: 798
Score: 317.00 Matches: 87
Percent Similarity: 51.00% Conservative: 41
Best Local Similarity: 34.66% Mismatches: 107
Query Match: 23.71% Indels: 16
DBs: 4 Gaps: 8

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US-10-063-735-128 (1-260) x US-09-328-352-2199 (1-798)

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QY 13 LeuAlaLeuValThrGlyAlaSerGlyGlyLeuAlaValAlaValAlaArgAlaLeuVal 32
DB 43 TTAGCATTTAGTTACAGGCGCATCAGCAGGTTTGGTTATAGTTATTTCAAAAAAACTGATT 102
QY 33 GlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIleGluGluLeuAla 52
DB 103 GAGTCAGGCTATAAAGTTATTGGATGTGGAAGCGCGAGAAAAAATTAGAAGAACTACAA 162
QY 53 AlaGluCysLysSerAlaGlyTyrProGlyThrLeuIleProTyrArgCysAspLeuSer 72
DB 163 AAACAGCTTGGCGAAAATTTCTACCCACTCGTATTT-----GATATGACT 207
QY 73 Asn---GluGluAspIleLeuSerMetPheSerAlaIleArgSer-----GlnHisSer 89
DB 208 GATACGGCAGAAAAATATAATAAGTTATTTAAAGAAATTTACCAATGAAATTTCAATCGAT 267
QY 90 GlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgPro---AspThrLeuLeuSer 108
DB 268 CAATTTGACTTACTAGTGAATAATGCAAGCTTGGCATTTGGCTTAGAGCCAGAGATAAA 327
QY 109 GlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCys 128
DB 328 GCGGATTTAGATGATTGGTACACCATGATTCATACCAATGTTAAAGCCCTTGTACGGTT 387
QY 129 ThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHisIleAsn 148
DB 388 ACCCGATTAAATTTTACCAAGTATGTTAAAGAGAAA-----TCAGGCTTAATCATTAA 441
QY 149 IleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPheTyrSerAla 168
DB 442 ATGGTTCAATTTGCGAGT-----ACATACCCATATCCAGGTGGTATGATATATGGGCA 495
QY 169 ThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGln 188
DB 496 ACAAAAGCTTTGTAGAGCAGTTTAGTTTAAATCTAGTCGAGATTG-----GCTGGT 549
QY 189 ThrHisIleArgAlaThrCysIleSerProGlyValVal---GluThrGlnPheAlaPhe 207
DB 550 ACTGGCTGCGGGTAACGAATATTAGCCAGGGTTGTGTGGTGTACCGAATTTTCTCTT 609
QY 208 LysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLysCysLeu 227
DB 610 GTACGTTTTAAGGAGATCAGGAGAAAGCTAACAGTCTATACGATATACGAAAAATCCAAT 669
QY 228 LysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGln 247
DB 670 TTGCGGAGAGATATTGCAATATACAGTAGCATGGATCGCATCACAAACCCGATATTAA 729

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Qy 248 IleGlyAspIleGlnMetArgProThrGluGln 258
 Db 730 ATTAACCGTATAGAAATGATCCACGACTCAG 762

RESULT 10
 US-09-134-001C-1560
 ; Sequence 1560, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 1560
 ; LENGTH: 696
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-1560

Alignment Scores:
 Pred. No.: 1,056-31 Length: 696
 Score: 316.50 Matches: 75
 Percent Similarity: 52.19% Conservative: 56
 Best Local Similarity: 23.88% Mismatches: 97
 Query Match: 23.67% Indels: 23
 DB: 4 Gaps: 7

US-10-063-735-128 (1-260) x US-09-134-001C-1560 (1-696)

Qy 6 MetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAla 25
 Db 4 ATGGCAAGATTAAAGAGAAAGTTCAGTCGTTACAGGTCGAGTAGCGGTATAGAGAG 63

Qy 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
 Db 64 GCGATTGCCAACAGTTAAGTCAACAAGTGCATCAATAGTCTCGTTGGTGTACGAA 123

Qy 46 GlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyProGlyThrLeuIle 65
 Db 124 CAACGCTTAAACGAAATAGTCCAGCAATTAAATAAC-----CCGCTAAAGTTGTT 174

Qy 66 ProTyArgCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArg 85
 Db 175 -----ACAGCGGATGTCATGTAAATCGAATAGATGATGTATTAAGCTGTATA 228

Qy 86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
 Db 229 GACCATTTGGTCATATCGATATTGTTGTAAGTAGCGAGGTCAAAGTTTATCATCTAAA 288

Qy 106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeu---Ala 124
 Db 289 ATTACAGACTATAATGTTGAGCAGTGGGATCTATGATAGATGTAATATTAAAGGTACA 348

Qy 125 LeuSerIleCysThrArgGluAlaTyGlnSerMetLysGluArgAsnValAspAspGly 144
 Db 349 CTCATGTTTACAGCGCATTCCTTATTTGTTTAAACAA-----TCTAGTGGG 399

Qy 145 HisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHis 164
 Db 400 CATATCATCAATCTTGCATCAGTATCAGGATTTGAA-----CCGACAAAGACGACGCC 453

Qy 165 PheTySerAlaThrIlystyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeu 184
 Db 454 GTTTATGGTGCACAAAGACGACCAATATCATGCAATCACACGTCTCTTGAAAGAAATTA 513

Qy 185 ArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGln 204
 Db 514 -----GCACGTACAGCGTTAAAGTACTAGTATTTTCCACGAGTAATGTTGATACC--- 564

Qy 205 PheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyGlnMet 224
 Db 565 -----CCTATGACGGAAGGACTGATTTTGGGGAACGC 597

Qy 225 LysCysLeuLysProGluAspValAlaGluAlaValIleTyValLeuSerThrProAla 244
 Db 598 AAAAAACTTGAAGCACAGAAATATTGCTGATATATGCTTTTAACACAACTAGT 657

Qy 245 HisIleGlnIleGlyAspIleGlnMetArgPro 255
 Db 658 CACGTTATGTTAATGAAGTAACGATAAGACCT 690

RESULT 11
 US-09-489-039A-6577
 ; Sequence 6577, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 6577
 ; LENGTH: 819
 ; TYPE: DNA
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-6577

Alignment Scores:
 Pred. No.: 1,536-30 Length: 819
 Score: 308.50 Matches: 83
 Percent Similarity: 48.39% Conservative: 37
 Best Local Similarity: 33.47% Mismatches: 115
 Query Match: 23.07% Indels: 13
 DB: 4 Gaps: 6

US-10-063-735-128 (1-260) x US-09-489-039A-6577 (1-819)

Qy 13 LeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAlaAlaValAlaArgAlaLeuVal 32
 Db 73 ATTATCATGTGCACCGCGCCACCGCGGTTTGTGGAAGTATTACTCGCGGTTTATFC 132

Qy 33 GlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIleGluGluLeuAla 52
 Db 133 GCTAACGGTCATAAAGTGAATGCCACCGGTCGCTGTGAAGCGGCTGAAGCGGTGAAA 192

Qy 53 AlaGluCysLysSerAlaGlyTyProGlyThrLeuIleProTyArgCysAspLeuSer 72
 Db 193 GACGAGCTGGCGGATAACCTTTATATCGCAACTT-----GACGTCGCG 237

Qy 73 AsnGluGluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAsp 92
 Db 238 AACCGCGCGCCCATGTGAGACGCTGATGCTGACCTGCGCGCGGAGTGGCGAGCTATCGAT 297

Qy 93 IleCysIleAsnAsnAlaGlyLeuAlaArgPro---AspThrLeuLeuSerGlySerThr 111
 Db 298 GTGCTGGTGAACAACCGCGCTGCGCTGTGTGTGGAGCGCGGCACCGCCAGTGTG 357

Qy 112 SerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGlu 131
 Db 358 GAAGACTGGGAAGATATGATCGACCAATAATAAAGGCGTGTGTACATGACCGCGGCC 417

Qy 132 AlaTyGlnSerMetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSer 151
 Db 418 GTGCTGCCGGGATGGTTGAGCGCAAT-----CCGCGCCATATCATCATATCGCTCT 471


```

; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
; STREET: The Jennifer Buliding, 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,614
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/790,462
; FILING DATE: 29-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: D. Douglas Price
; REGISTRATION NUMBER: 24,514
; REFERENCE/DOCKET NUMBER: 1418/P57452US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202 638-6666
; TELEFAX: (202) 39305350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-726-614-22

Alignment Scores:
Pred. No.: 1.52e-30 Length: 744
Score: 308.00 Matches: 78
Percent Similarity: 51.41% Conservative: 50
Best Local Similarity: 31.33% Mismatches: 111
Query Match: 23.04% Indels: 10
DB: 4 Gaps: 5

US-10-063-735-128 (1-260) x US-09-726-614-22 (1-744)

Qy 12 ArgLeuAlaLeuValThrGlyAlaSerGlyGlyLeuAlaValAlaArgAlaLeu 31
Db 723 AAGTCGCGCTCATCAGCGCGGAGCTCGGGCATCGGCGAGCCACGCGCGCCCTG 664
Qy 32 ValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIleGluLeu 51
Db 663 GCCGCGGAGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 604
Qy 52 AlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuLeuProTyrArgCysAspLeu 71
Db 603 GGTGACGAGCTGACCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 550
Qy 72 SerAsnGluGluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyVal 91
Db 549 GCCGACCGGAGGGGTGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 490
Qy 92 AspIleCysIleAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThr 111
Db 489 GACATCTCTCAACAACGCGCGGATCATCTGCTCGCGCGCGCGCGCGCGCGCGG 430
Qy 112 SerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGlu 131
Db 429 ACCGACTGGACCGGATGATCGACCACTCTCTGGGCGCTGATGATGATGATGATG 370
Qy 132 AlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHisIleIleAsnSer 151
Db 111
;

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Db 549 GCCGACCGGAGGGGTGGACCGCGCGTGCCTCCACCGTCCAGCGCGTGGCGGCGCTC 490
QY 92 AspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThr 111
Db 489 GACATCTCGTCAACACCGCGGGATCATGCTGCTCGCGCGGTGGAGGACGCCGACACC 430
QY 112 SerGlyTrpIysAspMetPheAsnValLeuAlaLeuSerIleCysThrArgGlu 131
Db 429 ACCGACTGACCGCGGATGATGACACCAATCTCTGGCGCTGATGACATGACCGGGCG 370
QY 132 AlaTyrGlnSerMetIysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSer 151
Db 369 GCCCTTCCCATCTGCTGGCG-----AGCAAGGGCACCCTGCTGCAGATGCTCTCG 319
QY 152 MetSerGlyHisArgValLeuProLeuSerValThrHisPheTyrSerAlaThrIysTyr 171
Db 318 ATCGCGGGCGG-----GTGAACGTCCGACGACGGCGCGTCTACAGCCACGAGTTC 265
QY 172 AlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIle 191
Db 264 GGTGTGAACCGCTTCAGCGAGCGTGGCGCAGGAGGTCAACGAG-----CGCGGGGTG 211
QY 192 ArgAlaThrCysIleSerProGlyValValGluThrGlnPheAlaPheIysLeu---His 210
Db 210 CGGGTGTGCTCATCGACCGCGGACCCACCGACACGAGCTCGCGCGGCCACATCACCCAC 151
QY 211 AspIysAspProGluIysAlaAlaAlaThrTyrGluGlnMetIysCysLeuIysProGlu 230
Db 150 ACCGCCACCAAGGAGATGATACGACGAGCGGATCAGCCAGATCCGCAAGTCCAGGCCGAG 91
QY 231 AspValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAsp 250
Db 90 GACATCGCGGAGGGGTCCGCTACCGCTGACCGCGCGCGCACCAACCGCTCCAGGCCGAG 31
QY 251 IleGlnMetArgProThrGluGlnVal 259
Db 30 ATCTTCATACGCGCCACCGACGAGTGC 4

RESULT 15
US-09-385-028-13/c
; Sequence 13, Application US/09385028
; Patent No. 6232106
; GENERAL INFORMATION:
; APPLICANT: Susan E. Jensen
; APPLICANT: Kwame A. Aidoo
; APPLICANT: Ashish S. Paradar
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
; Patent No. 6232106
; TITLE OF INVENTION: Acid Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, P.L.L.C.
; STREET: The Jennifer Building, 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/385,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/790,462
; FILING DATE: 29-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: D. Douglas Price
; REGISTRATION NUMBER: 24,514
; REFERENCE/DOCKET NUMBER: 1418/P57452US2

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 39305350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11604 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-385-028-13

Alignment Scores:
Pred. No.: 1,388-28 Length: 11604
Score: 308.00 Matches: 78
Percent Similarity: 51.41% Conservative: 50
Best Local Similarity: 31.33% Mismatches: 111
Query Match: 23.04% Indels: 10
DB: 3 Gaps: 5

US-10-063-735-128 (1-260) x US-09-385-028-13 (1-11604)
QY 12 ArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAlaValAlaArgAlaLeu 31
Db 11312 AAGTCGCGCTCATCACGGGCGGAGCTCGGGCATCGCGGAGGCCGCGCGCCCTG 11253
QY 32 ValGlnGlnGlyLeuIysValValGlyCysAlaArgThrValGlyAsnIleGluGluLeu 51
Db 11252 GCCGCGGAGGGCGCGCGTGGCCATCGCGGGCGCGGGTGCAGAACTGCGGCCCTG 11193
QY 52 AlaAlaGluCysIysSerAlaGlyTyrProGlyThrLeuIleProTyrArgCysAspLeu 71
Db 11192 GGTGACGAGCTGACCGCGCGGCGGAGGAGTCCATGTCCTC-----GAACCTGACGTC 11139
QY 72 SerAsnGluGluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyVal 91
Db 11138 GCCGACGCGGAGGGGTGGACGCGCGCTCCCTCCACCGTCCGAGCGCTGCGCGCCCTC 11079
QY 92 AspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThr 111
Db 11078 GACATCTCGTCAACACCGCGGATCATGCTGCTCGCGCGGTGGAGGACGCCGACACC 11019
QY 112 SerGlyTrpIysAspMetPheAsnValLeuAlaLeuSerIleCysThrArgGlu 131
Db 11018 ACCGACTGGACCGCGGATGATCGACCAATCTCTGGCGCTGATGATACATGACCCGGCG 10959
QY 132 AlaTyrGlnSerMetIysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSer 151
Db 10958 GCCCTTCCCATCTGCTGGCG-----AGCAAGGGCACCCTGCTGCAGATGCTCTCG 10908
QY 152 MetSerGlyHisArgValLeuProLeuSerValThrHisPheTyrSerAlaThrIysTyr 171
Db 10907 ATCGCGGGCGG-----GTGAACGTCCGCAACCGCGCGCTCTACAGGCCACCAAGTTC 10854
QY 172 AlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIle 191
Db 10853 GGTGTGAACCGCTTCAGCGAGACGCTCGCGCAGAGGTCAACCGAG-----CGCGGGGTG 10800
QY 192 ArgAlaThrCysIleSerProGlyValValGluThrGlnPheAlaPheIysLeu---His 210
Db 10799 CGGGTGTGCTCATCGAGCGGGCACCCACACGAGTGGCGCGGCCACATCACCCAC 10740
QY 211 AspIysAspProGluIysAlaAlaAlaThrTyrGluGlnMetIysCysLeuIysProGlu 230
Db 10739 ACCGCCACCAAGGATGTACGAGCAGCGGATCAGCCAGATCCGCAAGTCCAGGCCGAG 10680
QY 231 AspValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAsp 250
Db 10679 GACATCGCGGAGGGGTCCGCTACGCGGTGACCGCGCGCGCACCCACCGCGCGTCCAGG 10620
QY 251 IleGlnMetArgProThrGluGlnVal 259

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Db 10619 ATCTTCATACGCCCCCGACCGAGGTC 10593

Search completed: September 16, 2004, 17:59:02
Job time : 1112 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 11:18:21 ; Search time 115 Seconds
(without alignments)
713.346 Million cell updates/sec

Title: US-10-063-735-128
Perfect score: 1337
Sequence: 1 MARPGMRWRDLALVTGAS.....STPAHIQIGDIQMRTPEQVT 260

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SEPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	932	69.7	181	4	Q9BUC7	Q9buc7 homo sapien
2	924	69.1	181	4	Q9H674	Q9h674 homo sapien
3	864	64.6	181	11	Q8R249	Q8r249 mus musculus
4	482	36.1	251	5	Q9VYU9	Q9vyu9 drosophila
5	476	35.6	246	5	Q9VMH9	Q9vmh9 drosophila
6	442.5	33.1	250	5	Q9VZ19	Q9vz19 drosophila
7	441.5	33.0	250	5	Q8SY92	Q8sy92 drosophila
8	440	32.9	251	5	Q9XYM2	Q9xym2 drosophila
9	418.5	31.3	250	5	Q9VDC0	Q9vdc0 drosophila
10	407.5	30.5	248	5	Q9VD30	Q9vd30 drosophila
11	387.5	29.0	266	5	Q9VU92	Q9vu92 drosophila
12	380.5	28.5	200	5	Q95T88	Q95t88 drosophila
13	379	28.3	249	5	Q8IRN0	Q8irn0 drosophila
14	377	28.2	249	5	Q9SR56	Q9sr56 drosophila
15	375	28.0	256	16	Q8AAQ5	Q8aaq5 bacteroides
16	368	27.5	257	16	Q8YZ15	Q8yzi5 anabaena sp

17	363	27.2	258	16	Q83BJ5	Q83bj5 coxiella bu
18	355.5	26.6	273	16	Q9JUV3	Q9juv3 neisseria m
19	353.5	26.4	273	16	Q9JZR8	Q9jzr8 neisseria m
20	353	26.4	231	16	Q8NUV9	Q8nuv9 staphylococ
21	351	26.3	231	16	Q99RE5	Q99rf5 staphylococ
22	349.5	26.1	240	16	Q92X14	Q92xi4 rhizobium m
23	348.5	26.1	255	1	O34187	O34187 halobacteri
24	345	25.8	259	16	Q8FNO0	Q8fng0 corynebacte
25	336.5	25.2	253	16	Q83RE8	Q83re8 shigella fl
26	335.5	25.1	248	16	Q7UCH2	Q7uch2 shigella fl
27	334.5	25.0	244	16	Q8YV39	Q8yrv39 anabaena sp
28	334.5	25.0	253	16	Q8FHD2	Q8fhd2 escherichia
29	332	24.8	249	16	Q93OM2	Q93om2 rhizobium m
30	331.5	24.8	271	16	Q8UHZ8	Q8uhz8 agrobacteri
31	331	24.8	245	16	Q82ZU1	Q82zu1 enterococcu
32	331	24.8	248	16	Q88T73	Q88t73 lactobacill
33	328.5	24.6	248	16	Q8X505	Q8x505 escherichia
34	328.5	24.6	269	2	Q838D4	Q838d4 mycobacteri
35	327	24.5	248	2	Q9RH22	Q9rhd2 zymomonas m
36	326.5	24.4	253	16	Q97NV2	Q97nv2 streptococc
37	326	24.4	264	16	Q81M93	Q81m93 bacillus an
38	325.5	24.3	240	16	Q8X6K1	Q8x6k1 escherichia
39	325.5	24.3	260	17	Q9HSR4	Q9hsr4 halobacteri
40	324.5	24.3	249	2	Q9AGD6	Q9agd6 yersinia ps
41	323.5	24.2	244	16	Q55922	Q55922 synechocyst
42	323	24.2	239	16	Q87GP0	Q87gp0 vibrio para
43	322.5	24.1	230	16	Q8CN40	Q8cn40 staphylococ
44	321.5	24.0	245	16	Q9RJL6	Q9rjl6 streptomyce
45	320.5	24.0	249	2	Q93AP1	Q93ap1 yersinia ps

ALIGNMENTS

RESULT 1

Q9BUC7	PRELIMINARY;	PRT;	181 AA.
ID	Q9BUC7		
AC	Q9BUC7;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Uterus;		
RA	Strausberg R.;		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.		
DR	EMBL: BC002731; AAH02731.1; -		
DR	GO: GO:0016491; P:oxidoreductase activity; IEA.		
DR	GO: GO:0008152; P:metabolism; IEA.		
DR	InterPro: IPR002198; ADH short.		
DR	Pfam: PF00106; adh short; 1.		
DR	PRINTS: PR00080; SDRFAMILY.		
DR	PROSITE: PS00061; ADH_SHORT; 1.		
KW	Hypothetical protein; Oxidoreductase.		
SQ	SEQUENCE 181 AA; 20022 MW; 5BFCE5727835A38 CRC64;		

Query Match	69.7%;	Score 932;	DB 4;	Length 181;
Best Local Similarity	100.0%;	Pred. No. 2.1e-70;		
Matches 181;	Conservative	0;	Mismatches	0;
			Indels	0;
Qy	80	MFSAIRSQHSGVDICINNAGLARPDTLLSGTSGWKDMFNVLALSICTREAYQSMKER	139	
Db	1	MFSAIRSQHSGVDICINNAGLARPDTLLSGTSGWKDMFNVLALSICTREAYQSMKER	60	
Qy	140	NVDDGHLININSCHRVLPSTVTHYSATKYAVTALTEGLROELREAQTHIRATCISPG	199	

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Db 61 NVDDGHIINSMGSHRVLPVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 120
Qy 200 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 259
Db 121 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 180
Qy 260 T 260
Db 181 T 181

RESULT 2
Q9H674 PRELIMINARY; PRT; 181 AA.
AC Q9H674;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ22543.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohtsuka M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isono T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE EMBL/GenBank/DBJ databases.
CC SEQUENCE 181 AA; 19962 MW; 4EFCAB58978CE59D CRC64;

Query Match 69.1%; Score 924; DB 4; Length 181;
Best Local Similarity 99.4%; Pred. No. 9.9e-70;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 80 MFSAIRSQHSGVDICINNAGLARPDTLISGTSQGWKDMFNVLALSICTREAYQSMKER 139
Db 1 MFSAIRSQHSGVDICINNAGLARPDTLISGTSQGWKDMFNVLALSICTREAYQSMKER 60

Qy 140 NVDDGHIINSMGSHRVLPVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 199
Db 61 NVDDGHIINSMGSHRVLPVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 120

Qy 200 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 259
Db 121 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 180

Qy 260 T 260
Db 181 T 181

RESULT 3
Q8R249 PRELIMINARY; PRT; 181 AA.
AC Q8R249;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to hypothetical protein MGC4172.
OS Mus musculus (Mouse).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; BC022224; AAH22224.1; -.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
KW Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 181 AA; 19984 MW; 0791543F571EA43B CRC64;

Query Match 64.6%; Score 864; DB 11; Length 181;
Best Local Similarity 90.6%; Pred. No. 1.1e-64;
Matches 164; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 80 MFSAIRSQHSGVDICINNAGLARPDTLISGTSQGWKDMFNVLALSICTREAYQSMKER 139
Db 1 MFSAIRSQHSGVDICINNAGLARPDTLISGTSQGWKDMFNVLALSICTREAYQSMKER 60

Qy 140 NVDDGHIINSMGSHRVLPVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 199
Db 61 NIDGHIINSMGSHRVLPVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 120

Qy 200 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 259
Db 121 LVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 180

Qy 260 T 260
Db 181 T 181

RESULT 4
Q9VYU9 PRELIMINARY; PRT; 251 AA.
AC Q9VYU9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG9360 protein (RH17287p).
GN CG9360.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Db
1 MERQWKLAVVTGASGGIGAACARAWIGAGLRVVGGLARREAKLKL-RESLPRELQANFI 599
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Q9VMH9
ID Q9VMH9

66 PYRCDLSNEEDILSMFAIRSOHSGVDICINNAGLRDPDILLSGS-TSGWKDMFNVNILA 124
 60 PARCDVSKEDQVQSFDWIEREGADVLNNAGITRETELVTPSNTQKLKEVIDINVMG 119
 125 LSICITREAYQSMKERNVDGHHIININSMGHRVL-----PLSVTHFYSAKYAVTALTEGL 180
 120 VIWCTREAFNNMKRG-GECHVLVLIINISAGHQLNFDVLPSFNIPYATKFAITATTETY 178
 181 ROELREAOATHIRATCISGVVETOFAPKLHDKDPEKAAAYEQMKCLKPEDVAEAVIYL 240
 179 ROEFQLHGNKIRVTGICGAVNTNIF-----PEEIHFYVKOMARLEPANIADAVMYAL 231
 241 STPAHIQTGDI 251
 232 RTPPHVQSVII 242
 RESULT 6
 Q9VZ19 PRELIMINARY; PRT; 250 AA.
 ID Q9VZ19
 AC Q9VZ19;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ANTNDH protein.
 GN ANTNDH OR CG1386.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Aeburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Cocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan K.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Keenilson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laško P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J., Reese M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 PT "The genome sequence of Drosophila melanogaster."

Science 287:2185-2195(2000).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AE003485; AAF48012.1; -.
DR FlyBase; FBgn0026268; antdh.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 250 AA; 27279 MW; 790EE8F1DCADF025 CRC64;

Query Match 33.1%; Score 442.5; DB 5; Length 250;
Best Local Similarity 36.5%; Pred. No. 4.2e-29;
Matches 93; Conservative 56; Mismatches 91; Indels 15; Gaps 5;

QY 6 MERWRRLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGYPTLI 65
DB 1 MERQNRVAVVTGASGGIGSAIAKDLVLAGTVVGLARRVDRVKELQREL-PAEKGKLF 59
QY 66 PYRCDLSNBDILSMFSATRSQHSQVDICINNAGLARPDTLTLLSGSTSGWKDMFNVNVLAL 125
DB 60 ALYCDVGNSSVNEAFDWIILKLGALDVLVNNAGTLQPGYLVDMNPVAVMQVLTNIMGI 119
QY 126 SICTREAYOSMKERNVDDGHIININSMGSHRVLPISV-----THFYSATKYAVTALTEGL 180
DB 120 VLCTQRAVRSMRERKF-DGHVVLINSILGKTTWTATEGVAPDNNVPPSKHAVTALAEY 178
QY 181 ROELREAQTHIRATCSPGVVETQFAFLKHDKDPKAXAAAYEQMKCLKPEDVAEAVIYVL 240
DB 179 RQFFGLGTRIKITSVSPGVVDIEIV-----PDSIREAIKD-RMLHSEDIAGQVLIYAI 230
QY 241 STPAHIQIGDIQMRP 255
DB 231 ATPHVQVHELIKP 245

RESULT 7
Q8SY92 ID Q8SY92 PRELIMINARY; PRT; 250 AA.
AC Q8SY92; 2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RH21971P.
GN ANTDH OR CG1386.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Pohanuonavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RA Submitted (DRC-2001) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AY071705; AAL49327.1; -.
DR FlyBase; FBgn0026268; antdh.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 250 AA; 27265 MW; 6B9C78F1DCB2EF25 CRC64;

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Query Match          33.0%; Score 441.5; DB 5; Length 250;
Best Local Similarity 36.1%; Pred. No. 5.1e-29;
Matches 92; Conservative 57; Mismatches 91; Indels 15; Gaps 5;

QY 6 MERWRDLALVTGAGGIGAAVARALVQOGLKVGVGCARTVGNIEELAAECKSAGYPTLI 65
DB 1 MERWQNRVAVVTGASSGIGSAIAKDLVLGAGTVVGLARRVDRVKELQREL-PAEKRGKLF 59
QY 66 PYRCDLSNEEDILSMFSAIRSQHSQSGVDICINNAGLARPTLLSGTSGWKDMFNVLAL 125
DB 60 ALYCDVGNSSVNEAFDIIQKLGAIIDLVLNNAGTLPQGLVDMNPVAVMQVLTQNIIMI 119
QY 126 SICTREAYQSMKERNVDDGHIININSMGHRVPLSV-----THFYSATKYAVTALTEGL 180
DB 120 VLCTQRAVSRMRERKF-DGHVVVLINSILGHKTMWTATEGVAPDVNVYPPSKHVAITALAEGY 178
QY 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
DB 179 RQEFFGLGTRVKITSVSPGVWDTEIV-----PDSIREAIKD-RMLHSEIDIAQGVLYAI 230
QY 241 STPAHIQIGDQMRP 255
DB 231 ATPPHVQVHELIIKP 245

RESULT 8
Q9XV2 PRELIMINARY; PRT; 251 AA.
AC Q9XV2;
DT 01-NOV-1999 (TremBLrel. 12, Created)
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)
DE 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Antennal-specific short-chain dehydrogenase/reductase.
GN ANTDH OR CG1386.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S; TISSUE=Antenna;
RA Wang Q., Hasan G., Pikielny C.;
RT "Preferential Expression of Biotransformation Enzymes in the Olfactory
RT Organs of Drosophila melanogaster: the Antennae.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF116553; AAD22026.1; -.
DR FlyBase; FBgn0026268; antdh.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 251 AA; 27353 MW; 991A9BD7A4A9D0DB CRC64;

Query Match          32.9%; Score 440; DB 5; Length 251;
Best Local Similarity 36.5%; Pred. No. 6.8e-29;
Matches 93; Conservative 58; Mismatches 90; Indels 14; Gaps 5;

QY 6 MERWRDLALVTGAGGIGAAVARALVQOGLKVGVGCARTVGNIEELAAECKSAGYPTLI 65
DB 1 MERWQNRVSVVTGASSGIGSAIAKDLVLGAGTVVGLARRVDRVKELQREL-PAEKRGKLF 59
QY 66 PYRCDLSNEEDILSMFSAIRSQHSQSGVDICINNAGLARPTLLSGTSGWKDMFNVLAL 125
DB 60 ALYCDVGNSSVNEAFDIIQKLGAIIDLVLNNAGTLPQGLVDMNPVAVMQVLTQNIIMI 119
QY 126 SICTREAYQSMKERNVDDGHIININSMGHRVPLSV-----THFYSATKYAVTALTEGL 180
DB 120 VLCTQRAVSRMRERKF-DGHVVVLINSILGHKTMWTATEGVAPDVNVYPPSKHVAITALAEGY 178
QY 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
DB 179 RQEFFGLGTRVKITSVSPGVWDTEIV-----PDSIREAIKD-RMLHSEIDIAQGVLYAI 230
QY 241 STPAHIQIGDQMRP 255
DB 231 ATPPHVQVHELIIKP 245

RESULT 9
Q9VDC0 PRELIMINARY; PRT; 250 AA.
AC Q9VDC0;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE CG3301 protein (GH01837p).
GN CG3301.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George K.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Wang R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhou Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

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RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (DRC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL; AE003734; AAF55877.1; -;
 DR EMBL; AY069036; AAL39181.1; -;
 DR FlyBase; FBgn0038878; CG3301.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002198; ADH short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 KW Oxidoreductase.
 SQ SEQUENCE 250 AA; 27236 MW; 8C6892AFC62C4DF5 CRC64;
 Query Match 31.3%; Score 418.5; DB 5; Length 250;
 Best Local Similarity 38.2%; Pred. No. 4.3e-27;
 Matches 99; Conservative 50; Mismatches 87; Indels 23; Gaps 6;
 QY 6 MERWRDLALVTGASGGIGAAVARALVQOGLKVGVCARTVGNIEELAAECKS---AGYGP 62
 DB 1 MNRMLNRVAVVTGASAGIGAACCRDLVAKGMVVGGLARR----EKVLQDIKSSLPADQAA 56
 QY 63 TLIPYRCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLISGSTSG-WKDMFNVN 121
 DB 57 RFHTRPCDVNSQVQVITDFAWIDRTLGGADVLVNNAGIIRQWNTDPNSADVRAILDVN 116
 QY 122 VLALSICTREAYQSKMERNVDGHIININSMGHRVPLS--VTHFYSAKYAVTALTEG 179
 DB 117 VLGVWCTCRQWLSLQKRVNDGHVVLNSVVGHSVPAVEGSLNMYAPSKHAIITALTEI 176
 QY 180 LRQELREAQTHIRATCISPGVVEVTOFAFKLHDKDPEKAAATVEQ---MKCLKPEDVAEAV 236
 DB 177 LRQEPFKGTQTKITSISGVVATEIF-----EAGSWEQTPGMPMLRSEDIADAV 226
 QY 237 IYVLSTPAHIQIGDIQMP 255
 DB 227 TYCIQTPTPTVQIKELIIRP 245
 RESULT 10
 Q9VD30 PRELIMINARY; PRT; 248 AA.
 AC Q9VD30;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE CG7077 protein (GH05294p).
 GN CG7077.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandell W.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadenieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.-J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL; AE003738; AAF55973.1; -;
 DR EMBL; AY119471; AAM50125.1; -;
 DR HSPB; P14061; 1A27.
 DR FlyBase; FBgn0038946; CG7077.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002198; ADH short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 KW Oxidoreductase.
 SQ SEQUENCE 248 AA; 27265 MW; FDP1AF7C37155A70 CRC64;
 Query Match 30.5%; Score 407.5; DB 5; Length 248;
 Best Local Similarity 37.6%; Pred. No. 3.6e-26;
 Matches 97; Conservative 50; Mismatches 86; Indels 25; Gaps 6;
 QY 9 WRDLALVTGASGGIGAAVARALVQOGLKVGVCARTVGNIEELAAECKSAGYPTILPYR 68
 DB 7 WRNKVAVVTGASVGIGATTATIELANAGMVVVGGLARRVELIEALRDQVTGV---GKIFARQ 63
 QY 69 CDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLISGSTSGWKDMFNVNIALSIC 128
 DB 64 CDLNDEEQLASAFNWRKFOAIHVLIICNAGLKNFLESPTKIKELFDNINVTATSC 123
 QY 129 TREAYQSKMERNVDGHIININSMGHRV--LPLSVTHFYSAKYAVTALTEGLRQELRE 186
 DB 124 LREALKHAARKV-RGHIVVWNSVLGHRIPVPEVPLFSVYPATKHAITALCQTVRQEIHF 182
 QY 187 AQTHIRATCISPGVVEVTOFAFKLHDKDPEKAAATVEQ-----MKCLKPEDVAEAVIYVLT 242
 DB 183 LKLNKILTSICPGMVDTFD-----LSVYSQVAELPQLQARDVAKAVIYALNT 230
 QY 243 PAHIQIGDI---QMPTE 257
 DB 231 PDGVQVEDIILQOMRKVD 248

5

175 LEVLRLQELRGFKTKIKVT 192

Db

RESULT 13

Q81RNO PRELIMINARY; PRT; 249 AA.

AC Q81RNO

ID Q81RNO

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CG7090-PB.

GN CG10962 OR CG7090.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnikner S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

Abriel J.F., Agbayani A., An H.J., Andrews-Franknoch C., Baldwin D.,

BA Baller R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Beeson P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

FOsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Gleider A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hoslin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.R., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

Shue B.C., Sinden-Klamis I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.Y., Wasserman D.A., Weinstein G.W., Weissenbach J.,

Williams S.M., Woodgett W., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Smith H.O.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.

RT "The genome sequence of *Drosophila melanogaster*."

RL Science 287:2185-2195(2000).

RN [2]

SEQUENCE FROM N.A.

RP Celnikner S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phouanleavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

RA

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

RT "Sequencing of *Drosophila melanogaster* genome."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

SEQUENCE FROM N.A.

RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,

RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,

RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnikner S.E.,

RA Klomp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,

RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., S.E.;

RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;

RT "Annotation of *Drosophila melanogaster* genome."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

SEQUENCE FROM N.A.

RP Adams M.D., Celnikner S.E., Gibbs R.A., Rubin G.M., Venter J.C.;

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

SEQUENCE FROM N.A.

RP Flybase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB003445; AAF46428.1; --

DR FlyBase; FBGN0030073; CG10962.

DR GO; GO:0016491; P:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH short.

DR Pfam; PF00106; adh short; 1.

DR PRINTS; PR00080; SDRFAMILY.

SQ SEQUENCE 249 AA; 27141 MW; 8DAD823CEB7319AF CRC64;

Query Match 28.3%; Score 379; DB 5; Length 249;

Best Local Similarity 35.8%; Pred. No. 8.9e-24;

Matches 92; Conservative 55; Mismatches 88; Indels 22; Gaps 7;

Qy 6 MERWRDLALVTCAGSGTCAAVARALVOGLKVVGVCACTVGNIEE---LAAECKSAGYP 61

Db 1 MDRWQNRVAIVSGAGSGGACARLUVAAGLVQVGLARTDRLEQLRSLPAEQRMFH- 59

Qy 62 GTLIPYRCDSNEEDILSMFSAIRSQHSQVDCINAGLARPDTLGSGTSGWKDMFNVN 121

Db 60 ----QHKDVQSQELQVDTAFEMIEKELGIDVLINAGIVLGGQIDMPTKDINNILQTN 115

Qy 122 VLALSTCTREAVQSKERNVDDGHILINIS---MSGHVLPLSVT-HFYSATKYAVTALT 177

Db 116 LMGSICYCTKLAASSMRRRQV-AGHLIFVNSTAGVAGYKPDPADESLNATYTSKFTALTAVQ 174

Qy 178 EGLRQELREAQTHIRATCTISPGWETQPAFLKHDKDPKAAATYEQMKCLPDEVAEVI 237

Db 175 EICRQLINQSGKIKTSLNPGWATEIV-----PDETAKLGEV-ILQADDVAQVL 226

Qy 238 YVLSTPAHIQIGDIQWR 254

Db 227 YALSTPPTQVEQITLR 243

RESULT 14

Q95R56 PRELIMINARY; PRT; 249 AA.

ID Q95R56

AC Q95R56;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE SD06635P.

GN CG10962 OR CG7090.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

SEQUENCE FROM N.A.

RP Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 11:04:36 ; Search time 123 Seconds

(without alignments)
597.255 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMERWRDLALVTGAS.....STPAHIQIGDIQMRPTFQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1337	100.0	260	4	AAU29212	Human PRO
2	1337	100.0	260	4	AB84364	Amino aci
3	1337	100.0	260	4	AB87589	Human PRO
4	1337	100.0	260	5	AB95914	Human sec
5	1337	100.0	260	5	AAU76220	Human 216
6	1337	100.0	260	6	ABU58588	Human PRO
7	1337	100.0	260	6	ABU88136	Novel hum
8	1337	100.0	260	6	ABU84451	Human sec
9	1337	100.0	260	6	ABR66325	Human sec
10	1337	100.0	260	6	ABR65715	Human sec
11	1337	100.0	260	6	ABU99655	Human sec
12	1337	100.0	260	6	ABU82894	Human PRO
13	1337	100.0	260	6	ABU90015	Novel hum
14	1337	100.0	260	6	ABR68264	Human sec
15	1337	100.0	260	6	ABU96317	Novel hum
16	1337	100.0	260	6	ABU92748	Human sec
17	1337	100.0	260	6	ABO08825	Human sec
18	1337	100.0	260	6	ABO02877	Human sec
19	1337	100.0	260	6	ABR75031	Human sec
20	1337	100.0	260	6	ABR94793	Human sec
21	1337	100.0	260	6	ABU85766	Human PRO
22	1337	100.0	260	6	ABU98926	Novel hum
23	1337	100.0	260	6	ABU98141	Novel hum
24	1337	100.0	260	6	ABU91847	Novel hum
25	1337	100.0	260	6	ABU89540	Human PRO

ALIGNMENTS

RESULT 1

AAU29212
ID AAU29212 standard; protein; 260 AA.

XX AC AAU29212;

XX DT 18-DEC-2001 (first entry)

XX DE Human PRO polypeptide sequence #189.

XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX OS Homo sapiens.

XX PN WO200168848-A2.

XX PD 20-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006520.

XX PR 01-MAR-2000; 2000WO-US005601.

XX PR 02-MAR-2000; 2000WO-US005841.

XX PR 03-MAR-2000; 2000US-0187202P.

XX PR 06-MAR-2000; 2000US-0186968P.

XX PR 14-MAR-2000; 2000US-0189320P.

XX PR 15-MAR-2000; 2000US-0189328P.

XX PR 21-MAR-2000; 2000US-0190828P.

XX PR 21-MAR-2000; 2000US-0191007P.

XX PR 21-MAR-2000; 2000US-0191048P.

XX PR 28-MAR-2000; 2000US-0192655P.

XX PR 29-MAR-2000; 2000US-0193032P.

XX PR 30-MAR-2000; 2000US-0193053P.

XX PR 04-APR-2000; 2000WO-US008439.

XX PR 04-APR-2000; 2000US-0194449P.

XX PR 11-APR-2000; 2000US-0194647P.

XX PR 11-APR-2000; 2000US-0195975P.

XX PR 11-APR-2000; 2000US-0196000P.

XX PR 11-APR-2000; 2000US-0196187P.

XX PR 11-APR-2000; 2000US-0196690P.

XX PR 18-APR-2000; 2000US-0196820P.

XX PR 18-APR-2000; 2000US-0198121P.

XX PR 18-APR-2000; 2000US-0198585P.

XX PR 25-APR-2000; 2000US-0199397P.

ABU86381 Human sec
 ABU67594 Human sec
 ABU80622 Human PRO
 ABU90939 Novel hum
 ABO33998 Human sec
 ABR99540 Human sec
 ABR98930 Human sec
 ABO16453 Human sec
 ABR9353 Human sec
 ABO18994 Human sec
 ABR78415 Human sec
 ABU72015 Novel hum
 ABU85151 Novel hum
 ABO00290 Novel hum
 ABO11622 Human sec
 ABO02267 Human sec
 ABU88841 Novel hum
 ABU83536 Human sec
 ABO06337 Novel hum
 ABR59373 Human sec

PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-0064484B.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PA (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 FI N-PSDB; AAS46113.
 DR WPI; 2001-602746/68.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 11; Fig 378; 774pp; English.
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX Sequence 260 AA;
 SQ
 Query Match 100.0%; Score 1337; DB 4; Length 260;
 Best Local Similarity 100.0%; Pred. No. 1.7e-131;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARFGMRWRDLALVTGASGGIGAARALVQOGLKVVGCAITVGNIEELAAECKSAGY 60
 Db |||||||
 QY 61 PGTLLPYRCOLSNEDILSMFSATRSQSHGVYDICIINNAGLARPTLLSGSTSGWKDMFNV 120
 Db |||||||
 QY 61 PGTLLPYRCOLSNEDILSMFSATRSQSHGVYDICIINNAGLARPTLLSGSTSGWKDMFNV 120
 Db |||||||
 QY 121 NVLALSTCTRAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTEGL 180
 Db |||||||
 QY 121 NVLALSTCTRAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTEGL 180
 Db |||||||
 QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Db |||||||
 QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Db |||||||
 QY 241 STPAHIQIGDIQMRPTEQVT 260
 Db |||||||
 QY 241 STPAHIQIGDIQMRPTEQVT 260
 Db |||||||

RESULT 2
 AAB84364
 ID AAB84364 standard; protein; 260 AA.
 XX
 AC AAB84364;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Amino acid sequence of human alcohol dehydrogenase 21620.
 XX
 KW Human; alcohol dehydrogenase; colon disorder; brain disorder;
 KW skin disorder; heart disorder; blood vessel disorder; kidney disorder;
 KW prostate disorder; skeletal muscle disorder; ovary disorder;
 KW testis disorder; epididymis disorder; spleen disorder; lung disorder;
 KW liver disorder; uterus disorder; endometrium disorder; T-cell disorder;
 KW red cell disorder; thymus disorder; B cell disorder; breast disorder;
 KW thyroid disorder; pancreas disorder; small intestine disorder;
 KW reduced platelet number disorder; precursor T cell neoplasm.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 18..23
 FT /note= "putative N-myristoylation site"
 FT Modified-site 24..29
 FT /note= "putative N-myristoylation site"
 FT Modified-site 40..45
 FT /note= "putative N-myristoylation site"
 FT Modified-site 72..75
 FT /note= "putative casein kinase II phosphorylation site"
 FT Modified-site 89..92
 FT /note= "putative casein kinase II phosphorylation site"
 FT Modified-site 90..95
 FT /note= "putative N-myristoylation site"
 FT Modified-site 109..114
 FT /note= "putative N-myristoylation site"
 FT Modified-site 135..138
 FT /note= "putative casein kinase II phosphorylation site"
 FT Modified-site 135..137
 FT /note= "putative protein kinase C phosphorylation site"
 FT Region 166..176
 FT /note= "short-chain alcohol dehydrogenase family signature"
 FT Modified-site 199..204
 FT /note= "putative N-myristoylation site"
 XX
 PN WO200144446-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 15-DEC-2000; 2000WO-US033873.
 XX
 PR 15-DEC-1999; 99US-00464039.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Meyers R;
 XX
 XX WPI; 2001-390244/41.
 DR N-PSDB; AAB25131.
 XX
 XX Novel human alcohol dehydrogenase proteins, 21612, 21615, 21620, 21676,
 PT 33756, useful for treating psoriasis, tropical sprue, pancreatitis,
 PT Goiter, osteomalacia, endometriosis, angina pectoris, embolism.
 XX
 PS Claim 9; Fig 3; 156pp; English.
 CC
 CC AAB84364-68 represent human alcohol dehydrogenase proteins, designated
 CC 21620, 33756, 21676, 21612 and 21615, respectively. Alcohol dehydrogenase
 CC polynucleotides and polypeptides are useful for treatment and diagnosis
 CC of disorders mediated by or related to alcohol dehydrogenase. They can be
 CC used for treating disorders of colon, brain, skin, heart, blood vessels,
 CC kidney, prostate, skeletal muscle, ovary, testis and epididymis, spleen,

CC lung, liver, uterus and endometrium, T-cells, red cells, thymus, B cells,
CC breast, thyroid, pancreas, small intestine, reduced platelet number,
CC precursor T cell neoplasms, bone forming cells, and bone marrow cells
XX
SQ Sequence 260 AA;

Query Match 100.0%; Score 1337; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAREGMRWRDLALVTGASGGIGAAVARALVQGLKVVGCAARTVGNIEELAAECKSAGY 60
DB 1 MAREGMRWRDLALVTGASGGIGAAVARALVQGLKVVGCAARTVGNIEELAAECKSAGY 60
QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
DB 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTEGL 180
DB 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTEGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
DB 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 3

AAB87589
ID AAB87589 standard; protein; 260 AA.
XX
AC AAB87589;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1774.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO2000116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.

XX 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000US-0187202P.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-019397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.

(GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PU;
XX Grimaldi CJ, Gurney AL, Watanabe CK, Wood WT;
XX WPI; 2001-183260/18.

DR N-PSDB; AAF92121.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX

PS Claim 12; Fig 128; 278pp; English.

XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX

SQ Sequence 260 AA;

Query Match 100.0%; Score 1337; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAREGMRWRDLALVTGASGGIGAAVARALVQGLKVVGCAARTVGNIEELAAECKSAGY 60
DB 1 MAREGMRWRDLALVTGASGGIGAAVARALVQGLKVVGCAARTVGNIEELAAECKSAGY 60
QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
DB 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTEGL 180
DB 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTEGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
DB 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 4

ABG95914
ID ABG95914 standard; protein; 260 AA.
XX
AC ABG95914;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human secreted/transmembrane protein PRO1774.
XX
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.

XX 06-DEC-2001; 2001US-00006867.

PR 29-OCT-1997; 97US-0063435P.

PR 22-APR-1998; 98US-0082797P.

PR 15-MAY-1998; 98US-0085579P.

PR 02-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0088021P.

Db 181 RQELREAQTHIRATCISPGVVTQFAFKLHDKDPEKAATYEQMKCLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 5
AAU76220
ID AAU76220 standard; protein; 260 AA.
XX AC AAU76220;
XX DT 08-MAY-2002 (first entry)
XX DE Human 21620 alcohol dehydrogenase (ADH) protein.
XX KW Alcohol dehydrogenase; ADH; human; cytostatic; antiinflammatory;
KW cerebroprotective; anti-HIV; immunomodulator; hepatotropic; metastases;
KW pulmonary congestion; Meckel diverticulum; splenic infarction;
KW idiopathic inflammatory bowel disease; jaundice; cholestasis;
KW endometriosis; cerebral oedema; AIDS; leukopaenia; splenomegaly;
KW acquired immune deficiency disease; lupus erythematosus; dermatitis;
KW lung disease; adult respiratory distress syndrome; skin disease;
KW bronchitis; sarcoidosis; pneumothorax; colon disorder; colitis;
KW Crohn's disease; liver disorder; hepatitis; cirrhosis; brain disorder;
KW meningitis; Alzheimer's disease; Huntington's disease; atherosclerosis;
KW ischaemia; chromosome 17 (17q12-21); 21620; enzyme.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Region 166..176
XX FT /note= "Short chain ADH family signature"
XX PN US2002010946-A1.
XX PD 24-JAN-2002.

XX PF 28-FEB-2001; 2001US-00796089.
XX PR 15-DEC-1999; 99US-00464039.
XX PR 15-DEC-2000; 2000WO-US03873.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Meyers R;
XX DR WPI; 2002-179233/23.
XX DR N-PSDB; ABK15172.

XX FT New human alcohol dehydrogenase (ADH) polynucleotides and polypeptides,
XX FT useful as targets for diagnosing or treating ADH-related or ADH-mediated
XX FT disorders, e.g. malignant breast metastases, enema or leukopenia.
XX PS Claim 9; Fig 1A; 80pp; English.

XX CC This invention relates to the cDNA and protein sequences of 5 novel human
XX CC alcohol dehydrogenase molecules. The ADH polynucleotides and polypeptides
XX CC are useful as targets for diagnosing or treating ADH-related or ADH-
XX CC mediated disorders, e.g. malignant breast, liver, colon or liver
XX CC metastases, pulmonary congestion or enema, Meckel diverticulum,
XX CC idiopathic inflammatory bowel disease, jaundice and cholestasis,
XX CC endometriosis, cerebral oedema, AIDS, or leukopaenia. The sequences may
XX CC also be used for treating other diseases or disorders such as spleen
XX CC disorders (splenomegaly, splenic infarction), lung diseases (adult
XX CC respiratory distress syndrome, bronchitis, sarcoidosis, pneumothorax),
XX CC colon disorders (colitis, Crohn's disease), liver disorders (hepatitis,
XX CC cirrhosis), brain disorders (meningitis, Alzheimer's disease,
XX CC Huntington's disease), heart and blood vessel disorders (atherosclerosis,
XX CC ischaemia), skin diseases (lupus erythematosus, dermatitis) and many
XX CC other diseases listed in the specification. The polynucleotides and

CC polypeptides are also useful in screening methods to identify agonists
CC and antagonists for diagnosis or treatment. In particular, the
CC polypeptides and polynucleotides are useful in drug screening assays in
CC cell-based assays or cell-free systems, as well as for biological assays
CC related to ADHs. The ADH polypeptides are also useful for producing
CC antibodies specific for the ADH regions. The polynucleotides and
CC polypeptides may also be used for monitoring therapeutic effects during
CC clinical trials and other treatments. The present sequence represents the
CC human 21620 alcohol dehydrogenase protein of the invention the gene which
CC encodes this protein has been mapped to chromosome 17 (17q12-21)
XX SQ Sequence 260 AA;

Query Match 100.0%; Score 1337; DB 5; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARFGMERWRDLALVTGASGGIGAARALVQOGLKVVGCAATVGNIEELAAECKSAGY 60
Db 1 MARFGMERWRDLALVTGASGGIGAARALVQOGLKVVGCAATVGNIEELAAECKSAGY 60
QY 61 PGTILPYRCDLNSEDILSMFSAIRSOHSGVDICINNAGLARPTLLSGSTSGWKDMFNV 120
Db 61 PGTILPYRCDLNSEDILSMFSAIRSOHSGVDICINNAGLARPTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVPLSVTHFYSATKYAVTALTEGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVPLSVTHFYSATKYAVTALTEGL 180
QY 181 RQELREAQTHIRATCISPGVVTQFAFKLHDKDPEKAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 RQELREAQTHIRATCISPGVVTQFAFKLHDKDPEKAATYEQMKCLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 6
ABU59588
ID ABU58588 standard; protein; 260 AA.
XX AC ABU58588;
XX DT 15-APR-2003 (first entry)
XX DE Human PRO polypeptide #189.
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176492.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 21-OCT-1997; 97US-0063486P.
XX PR 24-OCT-1997; 97US-0063120P.
XX PR 24-OCT-1997; 97US-0063121P.
XX PR 28-OCT-1997; 97US-0063540P.
XX PR 28-OCT-1997; 97US-0063541P.
XX PR 28-OCT-1997; 97US-0063544P.
XX PR 28-OCT-1997; 97US-0063564P.
XX PR 29-OCT-1997; 97US-0063734P.
XX PR 31-OCT-1997; 97US-0063870P.
XX PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997;	97US-0065311P.	PR 17-JUN-1998;	98US-0089538P.
PR 21-NOV-1997;	97US-0086120P.	PR 17-JUN-1998;	98US-0089598P.
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PR	23-SEP-1998;	98US-0101477P.	PR	24-OCT-1997;	97US-0063120P.
PR	24-SEP-1998;	98US-0101738P.	PR	24-OCT-1997;	97US-0063121P.
PR	24-SEP-1998;	98US-0101739P.	PR	28-OCT-1997;	97US-0063540P.
PR	24-SEP-1998;	98US-0101739P.	PR	28-OCT-1997;	97US-0063541P.
PR	24-SEP-1998;	98US-0101743P.	PR	28-OCT-1997;	97US-0063544P.
PR	25-SEP-1998;	98US-0101922P.	PR	28-OCT-1997;	97US-0063564P.
PR	25-SEP-1998;	98US-0101786P.	PR	29-OCT-1997;	97US-0063734P.
PR	29-SEP-1998;	98US-0102207P.	PR	31-OCT-1997;	97US-0063870P.
PR	29-SEP-1998;	98US-0102240P.	PR	31-OCT-1997;	97US-0064103P.
PR	29-SEP-1998;	98US-0102330P.	PR	31-OCT-1997;	97US-0065311P.
PR	29-SEP-1998;	98US-0102331P.	PR	21-NOV-1997;	97US-0066120P.
PR	30-SEP-1998;	98US-0102487P.	PR	24-NOV-1997;	97US-0066466P.
PR	30-SEP-1998;	98US-0102570P.	PR	11-DEC-1997;	97US-0066772P.
PR	30-SEP-1998;	98US-0102571P.	PR	12-DEC-1997;	97US-0069335P.
PR	01-OCT-1998;	98US-0102684P.	PR	17-DEC-1997;	97US-0069425P.
PR	01-OCT-1998;	98US-0102687P.	PR	18-DEC-1997;	97US-0069870P.
PR	02-OCT-1998;	98US-0102965P.	PR	10-MAR-1998;	98US-007450P.
PR	06-OCT-1998;	98US-0103258P.	PR	11-MAR-1998;	98US-0077632P.
PR	06-OCT-1998;	98US-0103449P.	PR	11-MAR-1998;	98US-0077649P.
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Best Local Similarity					98US-0079664P.
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					98US-0079786P.
Qy	1	MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGY 60	PR	27-MAR-1998;	98US-0080107P.
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Qy	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLISGTSQGWKDPNV 120	PR	01-APR-1998;	98US-0080327P.
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Qy	121	NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTEGL 180	PR	08-APR-1998;	98US-0081049P.
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Qy	181	ROELREAQTHIRATCISPGVVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240	PR	09-APR-1998;	98US-0081195P.
Db	181	ROELREAQTHIRATCISPGVVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240	PR	15-APR-1998;	98US-0081838P.
Qy	241	STPAHIQIGDIQMRPTEQVT 260	PR	21-APR-1998;	98US-0082569P.
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AC	ABU88136;		PR	29-APR-1998;	98US-0083496P.
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XX	Human; secreted and transmembrane protein: PRO; gene therapy;		PR	06-MAY-1998;	98US-0084366P.
KW	tumour necrosis factor-alpha release; TNF-alpha release;		PR	07-MAY-1998;	98US-0084639P.
KW	chondrocyte proliferation; chondrocyte differentiation; tumour;		PR	07-MAY-1998;	98US-0084643P.
KW	adrenal tumour; lung tumour; colon tumour; breast tumour;		PR	15-MAY-1998;	98US-0085579P.
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.		PR	15-MAY-1998;	98US-0085582P.
OS	Homo sapiens.		PR	15-MAY-1998;	98US-008580P.
XX	US2003032127-A1.		PR	15-MAY-1998;	98US-008582P.
XX	13-FEB-2003.		PR	18-MAY-1998;	98US-0086023P.
XX	26-JUN-2002; 2002US-00183012.		PR	22-MAY-1998;	98US-0086392P.
XX	18-SEP-1997; 97US-0059263P.		PR	22-MAY-1998;	98US-0086486P.
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 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
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 PR 01-OCT-1998; 98US-0102684P.
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Query Match 100.0%; Score 1337; DB 6; Length 260;
 Best Local Similarity 100.0%; Pred. No. 1.7e-131;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERDRRLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
 DB 1 MARPGMERDRRLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60

QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMNV 120
 DB 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMNV 120

QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVLPVSVTHFYSATKYAVTALTGL 180
 DB 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVLPVSVTHFYSATKYAVTALTGL 180

QY 181 RQELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 DB 181 RQELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240

QY 241 STPAHIQIGDIQMRPTEQVT 260
 DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 8
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 ID ABUS4451 standard; protein; 260 AA.
 XX AC ABUS4451;
 XX DT 02-AUG-2003 (first entry)
 XX DE Human secreted/transmembrane protein (PRO) #189.
 XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
 XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 XX KW tissue typing.
 XX OS Homo sapiens.
 XX PN US2003032112-A1.

XX 13-FEB-2003.
PD 21-JUN-2002; 2002US-00176756.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
PF 17-OCT-1997; 97US-0062250P.
PF 21-OCT-1997; 97US-0063486P.
PF 24-OCT-1997; 97US-0063120P.
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PF 17-DEC-1997; 97US-0069870P.
PF 18-DEC-1997; 97US-0068017P.
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PR 12-JUN-1998; 98US-0089090P.
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PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
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PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
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PR 25-JUN-1998; 98US-0090694P.
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PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091344P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
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PR 02-JUL-1998; 98US-0091628P.
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PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
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PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
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PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.

PR	09-SEP-1998;	98US-0099602P.	DE	Human secreted polypeptide PRO1774, SEQ ID NO:378.
PR	10-SEP-1998;	98US-0099741P.	XX	
PR	10-SEP-1998;	98US-0099754P.	KW	Human; PRO; secreted protein; transmembrane protein;
PR	10-SEP-1998;	98US-0099763P.	KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
PR	10-SEP-1998;	98US-0099812P.	KW	chondrocyte; proliferation; differentiation; cartilage disorder;
PR	15-SEP-1998;	98US-0100388P.	KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
PR	16-SEP-1998;	98US-0100662P.	KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
PR	16-SEP-1998;	98US-0100664P.	KW	liver; drug screening; transgenic animal; genetic analysis;
PR	16-SEP-1998;	98US-0101751P.	KW	antiarthritic; vulnery; gene therapy.
PR	16-SEP-1998;	98WO-US019330.	XX	
PR	17-SEP-1998;	98US-0100683P.	OS	Homo sapiens.
PR	17-SEP-1998;	98US-0100684P.	XX	
PR	17-SEP-1998;	98US-0100919P.	PN	US2003027278-A1.
PR	17-SEP-1998;	98US-0100930P.	XX	
PR	18-SEP-1998;	98US-0100849P.	XX	
PR	18-SEP-1998;	98US-0101014P.	PD	06-FEB-2003.
PR	18-SEP-1998;	98US-0101068P.	XX	
PR	23-SEP-1998;	98US-0101471P.	XX	
PR	23-SEP-1998;	98US-0101472P.	XX	
PR	23-SEP-1998;	98US-0101475P.	XX	
PR	23-SEP-1998;	98US-0101477P.	XX	
PR	23-SEP-1998;	98US-0101738P.	XX	
PR	24-SEP-1998;	98US-0101739P.	XX	
PR	24-SEP-1998;	98US-0101743P.	XX	
PR	24-SEP-1998;	98US-0101922P.	XX	
PR	25-SEP-1998;	98US-0101786P.	XX	
PR	29-SEP-1998;	98US-0102207P.	XX	
PR	29-SEP-1998;	98US-0102240P.	XX	
PR	29-SEP-1998;	98US-0102330P.	XX	
PR	29-SEP-1998;	98US-0102331P.	XX	
PR	30-SEP-1998;	98US-0102487P.	XX	
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PR	30-SEP-1998;	98US-0102571P.	XX	
PR	01-OCT-1998;	98US-0102684P.	XX	
PR	01-OCT-1998;	98US-0102687P.	XX	
PR	02-OCT-1998;	98US-0102965P.	XX	
PR	06-OCT-1998;	98US-0103258P.	XX	
PR	06-OCT-1998;	98US-0103449P.	XX	
PR	07-OCT-1998;	98US-0016897P.	XX	
PR	07-OCT-1998;	98US-0059263P.	PR	18-SEP-1997;
PR	07-OCT-1998;	98US-0059266P.	PR	18-SEP-1997;
PR	07-OCT-1998;	98US-0062250P.	PR	17-OCT-1997;
PR	07-OCT-1998;	98US-0063486P.	PR	21-OCT-1997;
PR	07-OCT-1998;	98US-0063120P.	PR	24-OCT-1997;
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PR	07-OCT-1998;	98US-0063540P.	PR	28-OCT-1997;
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PR	07-OCT-1998;	98US-0063544P.	PR	28-OCT-1997;
PR	07-OCT-1998;	98US-0063734P.	PR	29-OCT-1997;
PR	07-OCT-1998;	98US-0063870P.	PR	31-OCT-1997;
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PR	07-OCT-1998;	98US-0065311P.	PR	13-NOV-1997;
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PR	07-OCT-1998;	98US-0066772P.	PR	24-NOV-1997;
PR	07-OCT-1998;	98US-0069335P.	PR	12-DEC-1997;
PR	07-OCT-1998;	98US-0069425P.	PR	12-DEC-1997;
PR	07-OCT-1998;	98US-0069870P.	PR	17-DEC-1997;
PR	07-OCT-1998;	98US-0068017P.	PR	18-DEC-1997;
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PR	07-OCT-1998;	98US-0077632P.	PR	11-MAR-1998;
PR	07-OCT-1998;	98US-0077649P.	PR	11-MAR-1998;
PR	07-OCT-1998;	98US-0078886P.	PR	20-MAR-1998;
PR	07-OCT-1998;	98US-0078939P.	PR	20-MAR-1998;
PR	07-OCT-1998;	98US-0079664P.	PR	27-MAR-1998;
PR	07-OCT-1998;	98US-0079786P.	PR	27-MAR-1998;
PR	07-OCT-1998;	98US-0080107P.	PR	31-MAR-1998;
PR	07-OCT-1998;	98US-0080194P.	PR	31-MAR-1998;
PR	07-OCT-1998;	98US-0080327P.	PR	01-APR-1998;
PR	07-OCT-1998;	98US-0080333P.	PR	01-APR-1998;
PR	07-OCT-1998;	98US-0081049P.	PR	08-APR-1998;
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PR	07-OCT-1998;	98US-0081195P.	PR	09-APR-1998;
PR	07-OCT-1998;	98US-0081838P.	PR	15-APR-1998;
PR	07-OCT-1998;	98US-0082568P.	PR	21-APR-1998;
PR	07-OCT-1998;	98US-0082569P.	PR	21-APR-1998;
PR	07-OCT-1998;	98US-0082704P.	PR	22-APR-1998;
PR	07-OCT-1998;	98US-0082797P.	PR	22-APR-1998;
PR	07-OCT-1998;	98US-0083322P.	PR	28-APR-1998;
PR	07-OCT-1998;	98US-0083495P.	PR	29-APR-1998;
PR	07-OCT-1998;	98US-0083496P.	PR	29-APR-1998;
PR	07-OCT-1998;	98US-0083499P.	PR	29-APR-1998;
PR	07-OCT-1998;	98US-0083559P.	PR	29-APR-1998;
PR	07-OCT-1998;	98US-0084366P.	PR	05-MAY-1998;
PR	07-OCT-1998;	98US-0084414P.	PR	06-MAY-1998;
PR	07-OCT-1998;	98US-0084639P.	PR	07-MAY-1998;
PR	07-OCT-1998;	98US-0084640P.	PR	07-MAY-1998;
PR	07-OCT-1998;	98US-0084643P.	PR	07-MAY-1998;
PR	07-OCT-1998;	98US-0085579P.	PR	15-MAY-1998;
PR	07-OCT-1998;	98US-0085580P.	PR	15-MAY-1998;
PR	07-OCT-1998;	98US-0085582P.	PR	15-MAY-1998;
PR	07-OCT-1998;	98US-0085700P.	PR	15-MAY-1998;
PR	07-OCT-1998;	98US-0086023P.	PR	18-MAY-1998;
QY	1 MARQMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAVTGNTIEELAAECKSAGY 60			
Db	1 MARQMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAVTGNTIEELAAECKSAGY 60			
QY	61 PGTLLPYRCDLSNEEDILSMFSAIRSQSHGVDCINNAGLARPTLLSGSTSGWKDMFNV 120			
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QY	121 NVLALSICTRAYOSMKERNVDDGHIININSMGHRVPLSVTHFYGATKYAVTALTEGL 180			
Db	121 NVLALSICTRAYOSMKERNVDDGHIININSMGHRVPLSVTHFYGATKYAVTALTEGL 180			
QY	181 RQELREAQTHIRATCISPGVWVETQAFKXLDKDEKAAATYEQMKCLKPEDVAEAVIYVL 240			
Db	181 RQELREAQTHIRATCISPGVWVETQAFKXLDKDEKAAATYEQMKCLKPEDVAEAVIYVL 240			
QY	241 STPAHIQIGDIQMRPTQVNT 260			
Db	241 STPAHIQIGDIQMRPTQVNT 260			
RESULT 9				
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XX				
AC	ABR66325;			
XX				
DT	05-AUG-2003 (first entry)			
XX				

PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0096959P.
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PR	28-MAY-1998;	98US-0087098P.	PR	26-AUG-1998;	98US-0097952P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097954P.
PR	02-JUN-1998;	98US-0087609P.	PR	26-AUG-1998;	98US-0097955P.
PR	02-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-0097971P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097974P.
PR	04-JUN-1998;	98US-0088025P.	PR	26-AUG-1998;	98US-0098014P.
PR	04-JUN-1998;	98US-0088028P.	PR	01-SEP-1998;	98US-0098716P.
PR	04-JUN-1998;	98US-0088029P.	PR	01-SEP-1998;	98US-0098723P.
PR	04-JUN-1998;	98US-0088033P.	PR	01-SEP-1998;	98US-0098803P.
PR	04-JUN-1998;	98US-0088326P.	PR	02-SEP-1998;	98US-0098821P.
PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-0098843P.
PR	05-JUN-1998;	98US-0088202P.	PR	09-SEP-1998;	98US-0098602P.
PR	05-JUN-1998;	98US-0088212P.	PR	10-SEP-1998;	98US-0099741P.
PR	05-JUN-1998;	98US-0088217P.	PR	10-SEP-1998;	98US-0099754P.
PR	09-JUN-1998;	98US-0088655P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088738P.	PR	15-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100684P.
PR	10-JUN-1998;	98US-0088824P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088825P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088826P.	PR	17-SEP-1998;	98US-0100683P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100919P.
PR	11-JUN-1998;	98US-0088876P.	PR	17-SEP-1998;	98US-0100930P.
PR	12-JUN-1998;	98US-0089090P.	PR	18-SEP-1998;	98US-0100849P.
PR	12-JUN-1998;	98US-0089105P.	PR	18-SEP-1998;	98US-0101014P.
PR	16-JUN-1998;	98US-0089512P.	PR	18-SEP-1998;	98US-0101068P.
PR	16-JUN-1998;	98US-0089514P.	PR	23-SEP-1998;	98US-0101471P.
PR	17-JUN-1998;	98US-0089538P.	PR	23-SEP-1998;	98US-0101472P.
PR	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101475P.
PR	17-JUN-1998;	98US-0089653P.	PR	23-SEP-1998;	98US-0101477P.
PR	18-JUN-1998;	98US-0089908P.	PR	24-SEP-1998;	98US-0101738P.
PR	19-JUN-1998;	98US-0089952P.	PR	24-SEP-1998;	98US-0101739P.
PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101743P.
PR	22-JUN-1998;	98US-0090252P.	PR	24-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090254P.	PR	25-SEP-1998;	98US-0101786P.
PR	24-JUN-1998;	98US-0090429P.	PR	25-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102240P.
PR	24-JUN-1998;	98US-0090444P.	PR	29-SEP-1998;	98US-0102330P.
PR	24-JUN-1998;	98US-0090461P.	PR	29-SEP-1998;	98US-0102331P.
PR	24-JUN-1998;	98US-0090535P.	PR	30-SEP-1998;	98US-0102487P.
PR	24-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102570P.
PR	25-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090690P.	PR	01-OCT-1998;	98US-0102687P.
PR	25-JUN-1998;	98US-0090694P.	Query Match 100.0%; Score 1337; DB 6; Length 260;		
PR	25-JUN-1998;	98US-0090695P.	Best Local Similarity 100.0%; Pred. No. 1.7e-131;		
PR	25-JUN-1998;	98US-0090696P.	Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
PR	26-JUN-1998;	98US-00105413.	Qy	1	MAREGMRWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
PR	26-JUN-1998;	98US-0090862P.	Db	1	MAREGMRWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
PR	26-JUN-1998;	98US-0090863P.	Qy	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
PR	26-JUN-1998;	98US-0091010P.	Db	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
PR	01-JUL-1998;	98US-0091359P.	Qy	121	NVLALSICTBEAYQSMKERNVDDGHIININMSGHVRVPLSVTHFYSATKYATVATL 180
PR	01-JUL-1998;	98US-0091544P.	Db	121	NVLALSICTBEAYQSMKERNVDDGHIININMSGHVRVPLSVTHFYSATKYATVATL 180
PR	02-JUL-1998;	98US-0091478P.	Qy	181	RQELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
PR	02-JUL-1998;	98US-0091486P.	Db	181	RQELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
PR	02-JUL-1998;	98US-0091628P.	Qy	241	STPAHIQIGDIQMRPTEQVT 260
PR	02-JUL-1998;	98US-0091632P.	Db	241	STPAHIQIGDIQMRPTEQVT 260
PR	24-JUL-1998;	98US-0094006P.	Qy		
PR	04-AUG-1998;	98US-0095282P.	Db		
PR	10-AUG-1998;	98US-0095998P.	Qy		
PR	10-AUG-1998;	98US-0096012P.	Db		
PR	17-AUG-1998;	98US-0096757P.	Qy		
PR	17-AUG-1998;	98US-0096766P.	Db		
PR	17-AUG-1998;	98US-0096867P.	Qy		
PR	17-AUG-1998;	98US-0096891P.	Db		
PR	18-AUG-1998;	98US-0096897P.	Qy		
PR	18-AUG-1998;	98US-0096949P.	Db		

RESULT 10
ABR65715
ID ABR65715 standard; protein; 260 AA.
XX
AC ABR65715;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1774, SEQ ID NO:378.
XX
KW Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
FN US2003036159-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00188773.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0052266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069333P.
PR 12-DEC-1997; 97US-0069423P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
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PR	29-SEP-1998;	98US-0102331P.	
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Qy	1	MARFGMRWRDLALVTGASGIGAAVARALVQGLKVGCAVTGNIIEELAAECKAGY	60
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Qy	61	PGTILPYRCOLSNEDILSMFSAIRSQHSGVDI CINNAGLARPTLLSGSTSGWKDMFNV	120
Db	61	PGTILPYRCOLSNEDILSMFSAIRSQHSGVDI CINNAGLARPTLLSGSTSGWKDMFNV	120
Qy	121	NVLALSICTREAYQSMKERNVDDGHHININSMGSHRVLPLSVTHFYSATKYAVTALTEGL	180
Db	121	NVLALSICTREAYQSMKERNVDDGHHININSMGSHRVLPLSVTHFYSATKYAVTALTEGL	180

Query Match 100.0%; Score 1337; DB 6; Length 260;

Best Local Similarity 100.0%; Pred. No. 1.7e-131;

Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	181	ROELREAQTHIRATCISPGVWETQFAFKLHDKDPKAAATYEQMKCLKPEDVAEAVIYVL	240
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Qy	241	STPAHIQIGDIQMRPTQVLT 260	
Db	241	STPAHIQIGDIQMRPTQVLT 260	
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ID	ABU99655	standard; protein; 260 AA.	
XX	AC	ABU99655;	
XX	DT	09-AUG-2003 (first entry)	
XX	DE	Human secreted/transmembrane protein (PRO) #189.	
XX	KW	Human; secreted and transmembrane protein; PRO; TNF-alpha;	
KW	KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	
XX	OS	tissue typing.	
XX	XX	Homo sapiens.	
PN	US2003040070-A1.		
XX	27-FEB-2003.		
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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1337; DB 6; Length 260;

Best Local Similarity 100.0%; Pred. No. 1,7e-131;

Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	PGTLIPYRCDLSNEEDIILSMFSATRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMENV	120	PR	09-APR-1998;	98US-00811195P.
Dd	61	PGTLIPYRCDLSNEEDIILSMFSATRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMENV	120	PR	15-APR-1998;	98US-0081838P.
Qy	121	NVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYFSATKYAVTALTEGL	180	PR	21-APR-1998;	98US-0082568P.
Dd	121	NVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYFSATKYAVTALTEGL	180	PR	21-APR-1998;	98US-0082569P.
Qy	181	QRELREAQTHIRATCISGVVETQFAFKLHKDPEKAAATYEQMKCLKPEDVAEAVIYVL	240	PR	22-APR-1998;	98US-0082704P.
Dd	181	QRELREAQTHIRATCISGVVETQFAFKLHKDPEKAAATYEQMKCLKPEDVAEAVIYVL	240	PR	22-APR-1998;	98US-0082704P.
Qy	241	STPAHIQIGDIQMPTEQVT	260	PR	28-APR-1998;	98US-0082797P.
Dd	241	STPAHIQIGDIQMPTEQVT	260	PR	28-APR-1998;	98US-0083322P.
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XX	AC	AC				98US-0083496P.
DT	27-JUN-2003	(first entry)				98US-0083496P.
DE	Human PRO polypeptide #189.					98US-0083496P.
XX	Human; PRO polypeptide; secreted and transmembrane protein; tumour;					98US-0083496P.
KW	chromosome mapping; gene mapping; cytostatic.					98US-0083496P.
KW						98US-0083496P.
XX	Homo sapiens.					98US-0083496P.
XX						98US-0083496P.
PN	US2003032113-A1.					98US-0083496P.
XX						98US-0083496P.
PD	13-FEB-2003.					98US-0083496P.
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PF	20-JUN-2002; 2002US-00176911.					98US-0083496P.
XX						98US-0083496P.
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PR	18-SEP-1997;	97US-0059266P.				98US-0083496P.
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PR	21-OCT-1997;	97US-0063486P.				98US-0083496P.
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QY 61 PGTLLPYRCDLNNEEDILSMFSAIRSQHSGYVDICINNAGLARPDPTLLSGSTSGWKDMENV 120
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QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFYSATKYAVTALTGL 180
DB 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFYSATKYAVTALTGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
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QY 241 STPAHIQIGDIQMRPTEQVT 260
DB 241 STPAHIQIGDIQMRPTEQVT 260
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KW chondrocyte differentiation; tumour necrosis factor-alpha release;
KW affinity purification.
OS Homo sapiens.
PN US2003036147-A1.
PD 20-FEB-2003.
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XX 02-JUL-2002; 2002US-00187741.
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Db 121 NVLALSICTRAYQSMKERNVDDGHIININSMGHRVLPPLSVTHFYFSATKYAVTALTEGL 180
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Db 241 STPAHIQIGDIOMRPTTEQVT 260

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XX AC ABR68264;
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XX DT 11-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO1774, SEQ ID NO:378.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX OS Homo sapiens.
XX XX
XX PN US2003027264-A1.
XX XX
XX PD 06-FEB-2003.
XX XX
XX PF 18-JUN-2002; 2002US-00174579.
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XX DT 25-JUL-2003 (first entry)
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XX KW knockout; chromosome identification; tissue typing; tumour;
XX KW chondrocyte proliferation; chondrocyte differentiation;
XX KW tumor necrosis factor-alpha release stimulator.
XX OS Homo sapiens.
XX PN US2003036144-A1.
XX PD 20-FEB-2003.
XX PF 01-JUL-2002; 2002US-00187601.
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Job time : 125 secs

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 14:46:16 ; Search time 3081 Seconds
(without alignments)
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	637	47.6	1715	3	AK116054	Ciona int
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19	441.5	33.0	965	3	AY071705	Drosophil
20	440	32.9	973	3	AF116553	Drosophil
21	439	32.8	1221	3	AY060282	Drosophil
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26	406.5	30.4	168583	3	AC104510	Drosophil
27	406.5	30.4	180919	2	AC007521	Drosophil
28	406.5	30.4	283075	3	AE003485	Drosophil
29	406.5	30.4	334028	2	AC116537	Drosophil
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ALIGNMENTS

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VERSION      BC002731.2 GI:33877092
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STRausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalilus,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE      22388257
PUBMED      12477932
2 (bases 1 to 1501)
STRausberg,R.
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12803782.
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgrl.nih.gov
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 AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
 Wood,W.I.
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 DEFINITION Sequence 377 from Patent WO0168848.
 ACCESSION AX376310
 VERSION AX376310.1 GI:19170546
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
 Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
 Zhang,Z.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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 JOURNAL Patent: WO 0168848-A 377 20-SEP-2001;
 Genentech, Inc. (US)
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			

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JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
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Score:	1337.00	Matches:	260
Percent Similarity:	100.00%	Conservative:	0
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Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal	120
Db	412	GCCGGGCTGACACCCCTCTCTCAGGACAGCCAGTGGTGAAGGACATGTTCAATGTG	471
Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
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Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
Db	592	TCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCTGCGCCACCGAGTGTACCCCTG	651
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
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ACCESSION AXI179289
VERSION AXI179289.1 GI:14598959
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Meyers, R.
21612, 21615, 21620, 21676, 33756, novel human alcohol
dehydrogenases
Patent: WO 0144446-A 2 21-JUN-2001;
Milleminium Pharmaceuticals, Inc. (US)
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QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyr 60
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DEFINITION Sequence 109 from Patent WO02099917.
ACCESSION AXI768992
VERSION AXI768992.1 GI:32437160
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Guo, X., Fernandes, E., Li, L., Kekuda, R., Liu, Y., Leite, M.,
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Vernet, C.A., Ballinger, R.A., Malyankar, U.M., Tchernev, V.T.,
Blalock, A.D., Gusev, V.Y., Rastelli, L., Mezes, P.D., Ellerman, K.,
Heyes, M., Herrmann, J.L., Shinkets, R.A., Ioime, N., Pena, C.E.,
Shenoy, S.G., Taupier, R.J., Gerlach, V. and Gorman, L.
Human proteins and nucleic acids encoding same
Patent: WO 0209917-A 109 12-DEC-2002;
Curagen Corporation (US)
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		ORGANISM	Mus musculus
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		TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
		JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
		MEDLINE	22388257
		PUBMED	12477932
		REFERENCE	2 (bases 1 to 1398)
		AUTHORS	Strausberg, R.
		TITLE	Direct Submission
		JOURNAL	Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
		COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcdpaxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
		FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAC Plate: 25 Row: b Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: GenomesScan gene prediction, Similarity but not identity to protein. Location/Qualifiers 1..1398 /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090" /clone="MGC:18716 IMAGE:4219994" /tissue_type="Colon, normal, 5 month old male mouse." /clone_lib="NCI CGAP_Co24" /lab_host="DH105" /note="Vector: pCMV-SPORT6" 1..1398 /gene="BC022224" /note="synonym: MGC18716" /db_xref="LocusID:192570" /db_xref="MGI:2652816" 305..850 /codon_start=1
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		Db	61 GCCGTGGCCCGGCCCTGGTCCAGCAGGAGCTGAAGGTGGTGGGCTGGCCCGGACATGTG 120
		QY	46 GlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIle 65
		Db	121 GGCAACATCGAGGAGCTGGCTGGAATGTGAAGAGTGCAGGCTACCCCGGACATTTGATC 180
		QY	66 ProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArg 85
		Db	181 CCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCGT 240
		QY	86 SerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThr 105
		Db	241 TCTCAGCACAGCGGTGTGACATCTGCATCAACAATGCTGGCTTGGCCCGCCCTGACACC 300
		QY	106 LeuLeuSerGlySerThrSerGlyTrrLysAspMetPheAsnValAsnValLeuAlaLeu 125
		Db	301 CTGCTCTCAGGAGCAGCAGCGTGGTTGGAGGACATGTTCAATGTGAACGTCTGGCCCTC 360
		QY	126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
		Db	361 AGCATCTGCACACGGGAAGCCTACCATCCATGAAGAGCGGAATGTGGACGATGGGCAC 420
		QY	146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
		Db	421 ATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACATC 480
		QY	166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
		Db	481 TATATGTCACCAAGATATGCCGTCACTGGCTGTACAGAGGACTGAGGCAAGAGCTTCGG 540
		QY	186 GluAlaGlnThrHisIleArgAlaThr----- 194
		Db	541 GAGGCCACAGACCCACATCCGACCCAGTGGCAGCTTCGGAGGAGGAGGCCCTCGCGGA 600
		QY	194----- 194
		Db	601 TATCAGCAGCAGCATCACTGTGAAGCTGGGTTCTGTGGCTCCATCTCTCCCTCGACC 660
		QY	195-----CysIle 196
		Db	561 TCCCAAGACCTGGCAAGCTCAGCCCTCAGAGGCCCTCTCTGTGGCCCGAGTGCATC 720
		QY	197 SerProGlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLys 216
		Db	721 TCTCCAGGTGGTGAGACACAATTCGGCTTCAAACTCCAGCAAGGACCCCTGAGAAG 780
		QY	217 AlaAlaAlaThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaVal 236
		Db	781 GCAGCTGCCACCTATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGTGGCCCGAGGTGT 840
		QY	237 IleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThr 256
		Db	841 ATCTAGTCTCTAGCACCCCGCCACATCCAGATGGAGACATCCAGATGAGGCCACG 900
		QY	257 GluGln 258
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of unknown specificity [general function prediction only]"
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ORIGIN
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Pred. No.: 3,21e-106 Length: 1398
Score: 1257.00 Matches: 241
Percent Similarity: 96.15% Conservative: 9
Best Local Similarity: 92.69% Mismatches: 10
Query Match: 94.02% Indels: 0
DB: 10 Gaps: 0

US-10-063-735-128 (1-260) x BC022224 (1-1398)

QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 68 ATGACTAGAGCTGGCATGGAGCGGTGGCGGACCGGCTGGCACGTGTGACGGGACCTCG 127
QY 21 GlyGlyIleGlyAlaAlaValAlaAlaArgAlaLeuValGlnGlnGlyValValGly 40
Db 128 GGGGGCATCGGTGGCGCGGTGGCGCGGCATAGTCCAGCAGGAGACTGAAGGTTGTGGGT 187
QY 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 188 TGTGCCCGCACCGTTGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTAC 247
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 248 CCGGGGACTTTGATCCCTCAGATGTGACCTGTGCAATGAGGAGGACATCTCTCCATG 307
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 308 TTCTCAGCTGTCCGATCCAGCACAGTGGCTGGATATCTGCATCAACAATGCCGGCATG 367
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
Db 368 GCCCGGCTGACACCCCTGCTCTCGGCGAGCCAGCGGATGGAAGGACATGTTCAATGTG 427
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 428 AATGTGCTGGCCCTCAGCATCTGCATCGGAGGCTTATCAGTCCATGAAGAGCGGAAC 487
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 488 ATAGACACGGGCACATCATTAACATCAACAGCATGTGTGGCCACCGAGTCCACCCAC 547
QY 161 SerValThrHisPheTyrSerAlaThrIlystYrAlaValThrAlaLeuThrGluGlyLeu 180
Db 548 TCTGTGATCATCTTCTATGTGCGACCTAAGTATCCGCTCATCTGCATGCAGAGGAGTCT 607
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 608 AGGCAAGAGCTTCTGGAGGCCACAGCCATATCCGGGCCAGCTGTATCTCTCCAGGCTTG 667
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
Db 668 GTAGAGACAGATTCGCTTCAAACTCCATGACAAGGACCCCGGGGAAGCAGCTGCCACC 727
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 728 TATGAACACATAAAGTGTCTCAGACACGAGGACGTGGCTGAGGCTGTCTACGTCTCTT 787
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
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Db 788 AGCACACCCCCACATGTTTCAGGTTGGTGACATCCAGATGAGGCCCCACAGAGAGTGACC 847

RESULT 8
AK026196
LOCUS
DEFINITION
Homo sapiens cDNA: FLJ22543 fis, clone HSI00212.
ACCESSION
AK026196
VERSION
AK026196.1 GI:10438967
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1
Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1410)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="HSI00212"
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243..788
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LSTPAHIQIDIQMRPEQVT"

CDS

ORIGIN

Alignment Scores:
Pred. No.: 3,18e-92 Length: 1410
Score: 1105.00 Matches: 221
Percent Similarity: 91.84% Conservative: 4
Best Local Similarity: 90.20% Mismatches: 16
Query Match: 82.65% Indels: 4
DB: 9 Gaps: 2

US-10-063-735-128 (1-260) x AK026196 (1-1410)

QY 20 SerGlyGlyIle-----GlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLys 37
Db 51 TCTGGTGGGTCTAGGCGCGCATGCCACCAAGCAGGTTCGCGCGCGGCGGAGAGCGG 110
QY 38 -----ValValGlyCysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCys 55
Db 111 CCGGGGCTGAGTCTCTCGACCCCGCTGTCGGGCAACATCGAGGAGCTGGCTGCTGAATGT 170
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Qy 56 LysSerAlaGlyTyrProGlyThrIleuLeuProTyrArgCysAspLeuSerAsnGluGlu 75
Db 171 AAGAGTCAGGCTACCCGGGACTTTGATCCCTACAGATGACCTATCAAAATGAAGAG 230
Qy 76 AspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIle 95
Db 231 GACATCTCTCCATGCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATC 290
Qy 96 AsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLys 115
Db 291 AACAAATGCTGGCTTGGCCGCGCTGACACCTGCTCTCAGGAGCAGCAGTGGTGAAG 350
Qy 116 AspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSer 135
Db 351 GACATGTTCAATGTGAACGTGCTGCCCTCAGCATCTGCACACCGGAGCCTACAGTCC 410
Qy 136 MetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHis 155
Db 411 ATGAAGAGCGGAATGTGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCAC 470
Qy 156 ArgValLeuProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAla 175
Db 471 CGAGTGTACCCCTCTCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACCTGC 530
Qy 176 LeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCys 195
Db 531 CTGACAGAGGAGCTAGGCAAGAGCTTCGGAGGCGCCAGACCCATCCGAGCCACGTGC 590
Qy 196 IleSerProGlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGlu 215
Db 591 ATCTCTCAGGTGTGGTGAGACACAAATCGCTTCAAACTCCAGACAGGACCTGAG 650
Qy 216 LysAlaAlaAlaThrTyrGluGlnMetLysCysLysLeuLysProGluAspValAlaGluAla 235
Db 651 AAGGAGCTGCCACCTATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCT 710
Qy 236 VallIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgPro 255
Db 711 GTTATCTACGTCTCAGACCCCGCCACACATCCAGATTGGAGACATCCAGATGAGGCC 770
Qy 256 ThrGluGlnValThr 260
Db 771 ACGGAGCAGGTGACC 785

RESULT 9
AC017377
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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FEATURES

source
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ORIGIN

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Pred. No.: 4.86e-49 Length: 1715
Score: 637.00 Matches: 121
Percent Similarity: 68.38% Conservative: 52
Best Local Similarity: 47.83% Mismatches: 76
Query Match: 47.64% Indels: 4
DB: 3 Gaps: 2

US-10-063-735-128 (1-260) x AK116054 (1-1715)

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Qy 6 MetGluArgTTPArgAspArgLeuAlaLeuValThrGlyAlaSerGlyIleGlyAla 25
Db 12 ATGGATAGGTGGATAGTAAGTTGCTATCTCTCAGGAGCTATGAAGGCATTTGGTGA 71
Qy 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db 72 GCAACTGTAAAAAGTTGGTCAGTCATGGAATGAAAGTGGTTGGTTGTCAAGAAATGAG 131
Qy 46 GlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrIleuLe 65
Db 132 GAAAACTGAAACAAATTCGCATCGGAAATCAACGGGAAGGTT--CAAGGGGAGATGTT 188
Qy 66 ProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArg 85
Db 189 CTTTCAAAATGTGATGTCAGATGAATCCACATCTTAGAAATGTTTAAATTTGTGAAG 248
Qy 86 SerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThr 105
Db 249 GAGAAGTTTGGAGCAGTACATCTGTGTTAATAATGCTGGGATAGCATTTGATTCTCCA 308
Qy 106 LeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeu 125
Db 309 ATATCATCGGAGACTCACAGAAATGGAAGAGAATCTTGGACACCAATGTTCTTGGTCTC 368
Qy 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
Db 369 AGCATCTGTTCCCGTGAAGCAGTACAACTAATGAAGAGACTGGAGTCGACGATGGCAT 428
Qy 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
Db 429 ATAGTTAATATCAATAGTGTGGTGCACAGGGTGGTGGACAAAGCCAAATG----- 479
Qy 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
Db 480 TATGCTGCATCTAAGTTTGCAGTCACTGCTCTTACTGAAGGTCTAAGAAGAGAGTTCGT 539
Qy 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
Db 540 TCTGCAAAATACATCATATTTCGTACAACTTCAATTTCCACGAGGCTATGTCAAAACGAAAT 599
Qy 206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
Db 600 TTTCAAAAATTTTACCAGACGACACTGAATGCGTCGAAATAATCTCTGAAATCTGTTAAA 659
Qy 226 CysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHis 245
Db 660 TGCCTTGAAGGTGAAGATATTGCTGCTGTGTGTATGTCAGTGTCCGACCTCTCAT 719
Qy 246 IleGlnIleGlyAspIleGlnMetArgProThrGluGln 258
Db 720 GTTGATATTATGAGATTATCATACGACCTGTGTGACCA 758

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RESULT 10

AC017377

LOCUS

AC017377 140468 bp DNA linear HTG 09-DEC-1999

Qy	177	ThrGluGlyLeuArgGlnGlnLeuArgGluAlaGlnThrHisileArgAlaThrCysIle	196
Db	33130	ACAGAGACATATCGGCAGGAATTTTCAGCTGCATCGACCAAAATCGGGTTACTGCATC	33189
Qy	197	SerProGlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLys	216
Db	33190	TGTCCTGTGTCGGTGACACGACGACATCTTC-----CCGGAAGAG	33228
Qy	217	AlaAlaAlaThrTyrrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaVal	236
Db	33229	ATCCATTTTACGTCAAGAGCTGCGGCAGACTCGAACCGACCAATCGGCAGCAGTG	33288
Qy	237	IleTyrrValLeuSerThrProAlaHisIleGlnIleGlyAspIle	251
Db	33289	ATGTATGCTCTCGCAACTCGCCTCATGTTTCAGGTGAGCATATC	33333

RESULT 11

AC004758

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

COMMENT

TITLE

JOURNAL

COMMENT

FEATURES

source

174311 bp DNA linear INV 29-MAY-1999

Drosophila melanogaster DNA sequence (pls DS06106 (D123), DS05973 (D122), and DS0584 (D118)), complete sequence

AC004758 AC004418 AC003710 AC002609 AC002610 AC002611 AC002612

AC002613 AC002614 AC002615 AC002616 AC002617 AC002618 AC003132

AC002619 AC004270 AC001713 AC001714 AC001715 AC001716 AC002591

AC001717 AC002592 AC002593 AC002594 AC002595 AC002596 AC001718

AC001719 AC002597 AC002598 AC002599 AC001720 AC001721 AC002600

AC001722 AC002601 AC001724 AC001725 AC002602 AC002603 AC001725

AC001726 AC002604 AC002605 AC002606 AC002607 AC002608 AC001727

AC004268 AC002583 AC003706 AC002584 AC002585 AC003707 AC003708

AC004758.1 GI:3168618

HTG.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 174311)

Celniker,S.E., Aghavani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B., Lomocan,M.A., Mazda,P., Mok,M.S., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,D., Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and Kimmel,B.

Sequencing of Drosophila chromosome 2L, region 26A5-26B5

Unpublished (1997)

2 (bases 1 to 174311)

Celniker,S.E., Aghavani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B., Lomocan,M.A., Mazda,P., Mok,M.S., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,D., Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and Kimmel,B.

Direct Submission

Submitted (29-MAY-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US

Sequence submitted by:

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (<http://fruitfly.berkeley.edu/sequence-archive.html>) or send email to drosophila@hgsc.lbl.gov.

Library locations: 58 64, 21 63, 40 90.

Location/Qualifiers

1..174311

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/mol_type="genomic DNA"

/db_xref="taxon:7227"

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ORIGIN									
Alignment Scores:									
Pred. No.:		2.13e-32		Length:		174311			
Score:		483.00		Matches:		107			
Percent Similarity:		60.39%		Conservative:		47			
Best Local Similarity:		41.96%		Mismatches:		87			
Query Match:		36.13%		Indels:		14			
DB:		3		Gaps:		5			
US-10-063-735-128 (1-260) x AC004758 (1-174311)									
QY	2	AlaArgProGlyMetGluArgTirPargAspArgLeuAlaLeuValThrGlyAlaSerGly	21						
Db	21538	TCACAAGACGGCATGGAGCGGTGCAGAACAACTGGCTGGTAACAGGAGCCAGCGGA	21597						
QY	22	GlyTleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCys	41						
Db	21598	GGCATAGCGCGCTGTGTCTCGGCCCATGATCGCGCTGCACTACGGGTGGTGGCCCTG	21657						
QY	42	AlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrPro	61						
Db	21658	GCACGTCCGGAGGCCAAGTTGAAGAGCTC---AGGAGAGCTCGCCCGGAGCTGCAG	21714						
QY	62	GlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPhe	81						
Db	21715	CGCAACTTCATACCGCGCGCTGCACGTCTCCAAGGAAGATCAGGTGCAGAGCTCTTT	21774						
QY	82	SerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAla	101						
Db	21775	GACTGGATCGAACGGGAGCTGGAGCGCCGACGCTGCTGCAACATGCTGGCATYACT	21834						
QY	102	ArgProAspThrLeuLeuSerGlySer---ThrSerGlyTyrLysAspMetPheAsnVal	120						
Db	21835	CGCAGACGGAACGTGTACCCTGAGCAATACGCAGAAAGCTTAAGAGGTTCATAGACACC	21894						
QY	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140						
Db	21895	AACGTAATGGCGTGAATTTGGTGTACCCGCGAGGGCTTCAATAACATGAACGGCGAGGT	21954						
QY	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeu-----	158						
Db	21955	---GGCGAAGTTCAGTTCTCATCATCAACAGCATAGCGGACATCAGTGTCTCAACTTC	22011						
QY	159	-----ProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeu	176						
Db	22012	ATCGACGTTTGGCCATCGTTCAATATATATATATATATATATATATATATATATATAT	22071						
QY	177	ThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIle	196						
Db	22072	ACAGAGACATATCGGCAGGAATTCAGCTGCATCGAACAAATCCGGTTACTGGCATC	22131						
QY	197	SerProGlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLys	216						
Db	22132	TGTCCTGTGCGGTGAACACGACATCTTC-----CCGGAAGAG	22170						
QY	217	AlaAlaAlaThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaVal	236						
Db	22171	ATCCATTTTTACGTCAAGACATGGCCAGACTCGAACACCGGCAACATTCGGAGCCAGTG	22230						
QY	237	IleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIle	251						
Db	22231	ATGATATGCTCTGGAACCTCGCCTCANGTTTCAGGTGAGCATAATC	22275						
RESULT 12									
AC092216									
LOCUS		AC092216		174832 bp		DNA		linear	
DEFINITION		Drosophila melanogaster, chromosome 2L, region 25F-26A, BAC clone BACR10M11, complete sequence.							
ACCESSION		AC092216							
VERSION		AC092216.1		GI:14578097					
KEYWORDS		HTG.							
SOURCE		Drosophila melanogaster (fruit fly)							
ORGANISM		Drosophila melanogaster							
REFERENCE		1 (bases 1 to 174832)							
AUTHORS		Celniker, S.E., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Chumpe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferreira, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.							
TITLE		Sequencing of Drosophila chromosome 2L, region 25F-26A							
JOURNAL		Unpublished							
REFERENCE		2 (bases 1 to 174832)							
AUTHORS		Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Chumpe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferreira, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.							
TITLE		Direct Submission							
JOURNAL		Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US							
COMMENT		Sequence submitted by: Lawrence Berkeley National Laboratory, MS 64-121 Berkeley, CA 94720							
		This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu .							
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Percent Similarity:		60.39%		Conservative:		47		47	

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DEFINITION	Drosophila melanogaster chromosome 2L section 21 of 83 of the complete sequence.			
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ORGANISM	Drosophila melanogaster			
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REFERENCE	1 (bases 1 to 260673)			
AUTHORS	Adams, M.D., Celisner, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,			

AUTHORS
 CONSRM Direct Submission
 TITLE Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
 JOURNAL 6 (bases 1 to 260673)
 REFERENCE
 AUTHORS
 CONSRM Direct Submission
 TITLE Submitted (23-JAN-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
 JOURNAL
 COMMENT On Sep 16, 2002 this sequence version replaced gi:7297037.
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VERSION AY094912.1 GI:20151810
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Ephydroidea; Drosophilidae; Drosophila.
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Stapleton,M., Brokstein,P., Hong,L., Aobayani,A., Carlson,J.,
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Miranda,A., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S.,
Patel,S., Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Rubin,G.M.
and Celniker,S.
Direct Submission
Submitted (03-APR-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.

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SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 24222)
Adams,M. and Venter,J.C.
Direct Submission
Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10210603 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
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US-10-063-735-128 (1-260) x AC017403 (1-24222)
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Db 7863 CTCGGTGTGGGCATCACCCACAGGGTAATGGCGCTGATCTTCGTGCCATCTCGATACC 7804
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 7803 AATGCTCTGGCGGTTCGTGTGCACCCGCGAGGCTTCAATCACTCAAGAGACGCAAT 7744
Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeu----- 158
Db 7743 GTTAAACGATGGACACATCTGATTCACAGTGTGGCGGACACCCGGTGATCAACAAC 7684
Qy 159 ProLeuSerValThrHisPheThrSerAlaThrIlystYrAlaValThrAlaLeuThrGlu 178
Db 7683 CCAAGGCATCCATGGGCATGTATTCGCCATCGAAGTACCGAGTCACCGCTCTCCAGGAG 7624
Qy 179 GlyLeuArgGlnGluLeuArgGluAlaGlnThr----- 189
Db 7623 GTGCTGCTCAGGAGTTCACAAACAGACCCAGACGATTACGGTAAGTGGCGAG 7564
Qy 190 -----HisIle 191
Db 7563 AGAGAGATTAGCTTAAAGTTGACATTTGACATTTACCCCTTTTCCGATAAATATCCATTGT 7504
Qy 192 ArgAlaThr-CysIleSerProGlyValValGluThrGlnPheAlaPheLysLeuHisAs 211
Db 7503 GATTTTACAGAGCATCATGTCCTCCGTCGCGTGACCGAGATCATTCGACAAG----- 7452
Qy 211 pLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLysCysLeuLysProGluAs 231
Db 7451 -----GAGGCTCTCGTTGGCATTCGCCACTTTTCCAATGCTCCGCTCTGAGGA 7405
Qy 231 pValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIle 251
Db 7404 TGTGGCGCATGCCATTAGCTACTGCTATCCAGACCCCGCCAAATGTCCAGATTCACGAGCT 7345
Qy 251 eGlnMetArgPro 255
Db 7344 GACCATCAAGCCT 7332
```

Search completed: September 16, 2004, 17:43:06
Job time : 3249 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 16:26:21; Search time 356 Seconds

(without alignments)
3102.617 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMERWRDLALVTGAS.....STPAHQIGDIQMRPTEQVT 260

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool_p/US10063735/runat_15092004_103012_8500/app_query.fasta_1.455
-DB=N Geneseq 29Jan04 -Qfmt=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US10063735@cgn_1_1_708@runat_15092004_103012_8500 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 29Jan04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1337	100.0	1493	9 ADB47522	Adb47522 Human CDN
2	1337	100.0	1505	4 AAS46113	Aas46113 Human DNA
3	1337	100.0	1505	4 AAF92121	Aaf92121 Human PRO
4	1337	100.0	1505	6 ABS74441	AbS74441 Human CDN
5	1337	100.0	1505	7 ABX78716	Abx78716 Human PRO
6	1337	100.0	1505	7 ACA75688	Aca75688 Novel hum
7	1337	100.0	1505	7 ACA71168	ACA71168 Human sec
8	1337	100.0	1505	7 ACC87696	Acc87696 Human sec

9	1337	100.0	1505	7	ACC87082	Acc87082 Human sec
10	1337	100.0	1505	7	ACD04255	ACD04255 Human sec
11	1337	100.0	1505	7	ACA69586	ACA69586 CDNA enco
12	1337	100.0	1505	7	ACA90431	ACA90431 Novel hum
13	1337	100.0	1505	7	ACC89538	ACC89538 Human sec
14	1337	100.0	1505	7	ACA98329	ACA98329 Novel hum
15	1337	100.0	1505	7	ACA93971	ACA93971 Human sec
16	1337	100.0	1505	7	ACD15364	ACD15364 Human sec
17	1337	100.0	1505	7	ACD08951	ACD08951 Human sec
18	1337	100.0	1505	7	ACF96871	ACF96871 Human sec
19	1337	100.0	1505	7	ACF15592	ACF15592 Human sec
20	1337	100.0	1505	7	ACA72959	ACA72959 Human PRO
21	1337	100.0	1505	7	ACD03131	ACD03131 Novel hum
22	1337	100.0	1505	7	ACD01946	ACD01946 Novel hum
23	1337	100.0	1505	7	ACA92138	ACA92138 Novel hum
24	1337	100.0	1505	7	ACA89563	ACA89563 CDNA enco
25	1337	100.0	1505	7	ACA73573	ACA73573 Human sec
26	1337	100.0	1505	7	ACA05888	ACA05888 Human sec
27	1337	100.0	1505	7	ACA66722	ACA66722 CDNA enco
28	1337	100.0	1505	7	ACA91227	ACA91227 Novel hum
29	1337	100.0	1505	7	ACD81604	ACD81604 Human CDN
30	1337	100.0	1505	7	ACF20297	ACF20297 Human sec
31	1337	100.0	1505	7	ACF19683	ACF19683 Human sec
32	1337	100.0	1505	7	ACD21971	ACD21971 Human sec
33	1337	100.0	1505	7	ACF13136	ACF13136 Human sec
34	1337	100.0	1505	7	ACD25239	ACD25239 Human sec
35	1337	100.0	1505	7	ACF00288	ACF00288 Human sec
36	1337	100.0	1505	7	ACA60426	ACA60426 Novel hum
37	1337	100.0	1505	7	ACA72345	ACA72345 Novel hum
38	1337	100.0	1505	7	ACD04869	ACD04869 Novel hum
39	1337	100.0	1505	7	ACD18330	ACD18330 Human sec
40	1337	100.0	1505	7	ACD08337	ACD08337 Human sec
41	1337	100.0	1505	7	ACA88771	ACA88771 Novel hum
42	1337	100.0	1505	7	ACA70213	ACA70213 Human sec
43	1337	100.0	1505	7	ACD12435	ACD12435 Novel hum
44	1337	100.0	1505	7	ACC74350	ACC74350 Human sec
45	1337	100.0	1505	7	ACD15978	ACD15978 Human sec

ALIGNMENTS

RESULT 1
ADB47522
ID: ADB47522 standard; CDNA; 1493 BP.
XX
AC ADB47522;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human CDNA upregulated in dendritic cells SEQ ID NO 222.
XX
KW ss; gene; human; dendritic cells; high throughput; cancer;
KW infectious disease; autoimmune disease; allergy;
KW graft versus host disease; vaccine enhancing; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003134283-A1.
XX
PD 17-JUL-2003.
XX
PF 03-OCT-2001; 2001US-00971392.
XX
PR 03-OCT-2000; 2000US-0237652P.
XX
PA (PETE/) PETERSON D P.
PA (PEAR/) PEARSON C I.
XX (COCK/) COCKS B G.
XX Peterson DP, Pearson CI, Cocks BG;
XX WPI; 2003-662509/62.
XX

PT New combination comprises cDNAs that are differentially expressed in
PT dendritic cells useful for preparing a composition for diagnosing or
PT treating cancer, infectious disease, autoimmunity, allergy or graft
PT versus host disease.
PT

PS Claim 1; SEQ ID NO 222; 28bp; English.

The invention relates to a combination comprising cDNAs that are differentially expressed in dendritic cells (DC). Also included is a high throughput method for detecting differential expression of one or more cDNAs in a sample containing nucleic acids. The combination is useful for preparing a composition for diagnosing, treating and monitoring the treatment of cancer, infectious disease, autoimmunity, allergy or graft versus host disease, or for enhancing a vaccine. The present sequence represents a human cDNA upregulated in dendritic cells. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030134283.

Sequence 1493 BP; 297 A; 442 C; 419 G; 335 T; 0 U; 0 Other; XX

Alignment Scores:	
Pred. No.:	2.32e-128
Score:	1337.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Best Overall Similarity:	100.00%
Query Match:	100.00%
DB:	9
	Matches: 1493
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

US-10-063-735-128 (1-260) x ADB47522 (1-1493)

Qy	1	MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer	20
Db	112	ATGCCACGGCCGGCATGGACGGTGGCGCAGCCGGCTGGCGCTGGTACGGGGGCGCTCG	171
Qy	21	GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuIysValValGly	40
Db	172	GGGGGCATCGCGCGGCCGTGGCCGGGCCCTGGTCCAGCAGGAGCTGAAGGTGGTGGC	231
Qy	41	CysAlaArgThrValGlyAsnIleGluIleuAlaAlaGluCysIysSerAlaGlyTyr	60
Db	232	TGCCCCCGCATGTGGGCAACATCGAGAGGTGGTGTGTAATGTAAGAGTGCAGGCTAC	291
Qy	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
Db	292	CCCGGACTTGATCCCTCAGATGTGCACCTATCAATGAAGACGACATCTCTCCATG	351
Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100
Db	352	TTCTCAGCTATCCGTTCTCAGCACACGGGTGAGACATCTGCATCAACAATGCTGGCTTG	411
Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAsnMetPheAsnVal	120
Db	412	GCCCGGCTGACCCCTGCTCTCAGCAGACACCGTGTGAGAGACATGTTCAATGTG	471
Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
Db	472	AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCACTCCATGAAGCAGCGAAT	531
Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
Db	532	GTGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG	591
Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
Db	592	TCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGACTG	651
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
Db	652	AGGCAAGAGCTTCGGGAGGCCACCCACATCCCGAGCCACGTGCATCTCTCCAGGTGTG	711
Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr	220

Db	712	GTGAGACACAATTGGCTTCAAACTCCACGACAGGACCTTGAGAACGACGCTGCCACC	777
Qy	221	TyrGluGlnMetIysCysLeuLysProGluAspValAlaGluAlaValIleTyrValIleu	240
Db	772	TATGAGCAAAATGAAGTGCTCTCAAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCCTC	831
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260
Db	832	AGCACCCCGACACATCCAGATTGGAGACATCCAGATGAGGCCCCACGAGCAGGTGACC	891
RESULT 2			
AAS46113			
ID	AAS46113 standard; cDNA; 1505 BP.		
AC	AAS46113;		
XX	18-DEC-2001 (first entry)		
DT	Human DNA encoding PRO polypeptide sequence #189.		
DE	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;		
KW	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;		
KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;		
KW	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;		
KW	PCR primer.		
XX	Homo sapiens.		
OS	WO200168848-A2.		
XX	20-SEP-2001.		
XX	28-FEB-2001; 2001WO-US006520.		
XX	01-MAR-2000; 2000WO-US005601.		
PR	02-MAR-2000; 2000WO-US005841.		
PR	03-MAR-2000; 2000US-0187202P.		
PR	06-MAR-2000; 2000US-0186968P.		
PR	14-MAR-2000; 2000US-0189320P.		
PR	14-MAR-2000; 2000US-0189328P.		
PR	15-MAR-2000; 2000WO-US006884.		
PR	21-MAR-2000; 2000US-0190828P.		
PR	21-MAR-2000; 2000US-0191007P.		
PR	21-MAR-2000; 2000US-0191048P.		
PR	21-MAR-2000; 2000US-0191314P.		
PR	28-MAR-2000; 2000US-0192655P.		
PR	29-MAR-2000; 2000US-0193032P.		
PR	29-MAR-2000; 2000US-0193053P.		
PR	30-MAR-2000; 2000WO-US008439.		
PR	04-APR-2000; 2000US-0194449P.		
PR	04-APR-2000; 2000US-0194647P.		
PR	11-APR-2000; 2000US-0195975P.		
PR	11-APR-2000; 2000US-0196000P.		
PR	11-APR-2000; 2000US-0196187P.		
PR	11-APR-2000; 2000US-0196650P.		
PR	11-APR-2000; 2000US-0196820P.		
PR	18-APR-2000; 2000US-0198121P.		
PR	18-APR-2000; 2000US-0198585P.		
PR	25-APR-2000; 2000US-0199397P.		
PR	25-APR-2000; 2000US-0199550P.		
PR	25-APR-2000; 2000US-0199654P.		
PR	03-MAY-2000; 2000US-0201516P.		
PR	17-MAY-2000; 2000WO-US013705.		
PR	22-MAY-2000; 2000WO-US014042.		
PR	30-MAY-2000; 2000WO-US014941.		
PR	02-JUN-2000; 2000WO-US015264.		
PR	05-JUN-2000; 2000US-0209832P.		
PR	28-JUL-2000; 2000US-02020710.		
PR	22-AUG-2000; 2000US-00844848.		
PR	24-AUG-2000; 2000WO-US023328.		
PR	08-NOV-2000; 2000WO-US030952.		
PR	01-DEC-2000; 2000WO-US032678.		
PR	20-DEC-2000; 2000WO-US034956.		

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

XX PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX DR WPI; 2001-602746/68.

XX DR P-PSDB; AAU29212.

XX PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the

XX PT presence of tumors, such as prostate and breast tumors, in mammals and to

XX PT screen for modulators of the compounds.

XX PS Claim 2; Fig 377; 774pp; English.

XX CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR

XX CC primers for PRO polypeptides of the invention. The sequences of the

XX CC invention can be used to detect the presence of a tumour in a mammal by

XX CC comparing the level of expression of a PRO polypeptide in a test sample

XX CC of cells from the animal and a control sample of normal cells, whereby a

XX CC higher level of expression in the test sample indicates the presence of a

XX CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,

XX CC pigs, goats and rabbits but are preferably human. The polypeptides can be

XX CC used to stimulate tumour necrosis factor (TNF) alpha release from human

XX CC blood, when contacted with it. A specific polypeptide can be used to

XX CC stimulate the proliferation or differentiation of chondrocyte cells. The

XX CC PRO proteins can be used to determine the presence of tumours and also

XX CC susceptibility to tumour development, particularly adrenal, lung, colon,

XX CC breast, prostate, rectal, cervical, or liver tumours, in mammalian

XX CC subjects. The oligonucleotide probes specific for the PRO nucleic acids

XX CC can be used for genetic analysis of individuals with genetic disorders

XX SQ Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.35e-128 Length: 1505

Score: 1337.00 Matches: 260

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-063-735-128 (1-260) x AAS46113 (1-1505)

QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20

DB 112 ATGCCAGCGCCGGCATGGAGCGTGGCGCGACCGCGCTGGTGGCGGGGCGCTCG 171

QY 21 GlyGlyIleGlyAlaAlaValAlaAraAlaLeuValGlnGlnGlyLeuLysValValGly 40

DB 172 GGGGGCATCGCGCGCGCTGGCGCGCGCTGGTCCAGCAGGACTGAAGTGTGGGC 231

QY 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60

DB 232 TGCCTCCGCGCATGTGGGCAACATCCAGAGTGGCTGCTGAATGAAGAGTGCAGGCTAC 291

QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMet 80

DB 292 CCCGGGACCTTTGATCCCCCTCAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351

QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100

DB 352 TTCTCAGTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG 411

QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120

DB 412 GCCCGGCTGCACCCCTGCTCAGGAGCAGCAGTGGTGGAGGACATGTTCAATGTG 471

QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140

DB 472 AACGTGTGGCCCTCAGCATCTGCACACGGGAGCCCTACCATGTCATGAAGAGCGAAT 531

QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160

DB 532 GTGACGATGGCACATCATTAATAGCATGTCTGGCCACCGAGTGTATCCCTG 591

QY 161 SerValThrHisPheTyrSerAlaThrThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180

DB 592 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGACTG 651

QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200

DB 652 AGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCATGTCATCTCTCCAGTGTG 711

QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220

DB 712 GTGAGACACAAATTCGCTTCAAACTCCACAGAGGACCTGAGAGGAGTCCAC 771

QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240

DB 772 TATGAGCAATGAAGTGTCTCAACCCGAGGATGTGGCCGAGGCTGTATCTACGTCCTC 831

QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260

DB 832 AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGA 891

RESULT 3

AAF92121

ID AAF92121 standard; cDNA; 1505 BP.

XX AC AAF92121;

XX DT 15-MAY-2001 (first entry)

XX DE Human PRO1774 cDNA.

XX KW Human; PRO protein; mapping; ss.

XX OS Homo sapiens.

XX PN WO200116318-A2.

XX PD 08-MAR-2001.

XX PF 24-AUG-2000; 2000WO-US023328.

XX PR 01-SEP-1999; 99WO-US020111.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 07-DEC-1999; 99US-0169495P.

XX PR 09-DEC-1999; 99US-0170262P.

XX PR 11-JAN-2000; 2000US-0175481P.

XX PR 18-FEB-2000; 2000WO-US004341.

XX PR 18-FEB-2000; 2000WO-US004342.

XX PR 22-FEB-2000; 2000WO-US004414.

XX PR 01-MAR-2000; 2000WO-US005601.

XX PR 03-MAR-2000; 2000US-0187202P.

XX PR 21-MAR-2000; 2000US-0191007P.

XX PR 30-MAR-2000; 2000WO-US008439.

XX PR 25-APR-2000; 2000US-0199397P.

XX PR 22-MAY-2000; 2000WO-US014042.

XX PR 05-JUN-2000; 2000US-0209832P.

XX PA (GETH) GENENTECH INC.

XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX DR WPI; 2001-183260/18.

XX DR P-PSDB; AAB87589.

XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular

XX PT biology, including use as hybridization probes, and in chromosome and

XX PT gene mapping.

XX PS Claim 2; Fig 127; 278pp; English.

CC The present sequence is the coding sequence for a human PRO polypeptide
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
 CC antagonists or anti-PRO antibodies are useful for preparation of a
 CC medicament useful in the treatment of a condition which is responsive to
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
 CC protein may also be employed as molecular weight markers for protein
 CC electrophoresis. The PRO coding sequence has applications in molecular
 CC biology, including use as hybridisation probes, and in chromosome and
 CC gene mapping

XX SQ Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,35e-128	Length:	1505
Score:	1337.00	Matches:	260
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-063-735-128 (1-260) x AAF92121 (1-1505)

QY	1	MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer	20
DB	112	ATGCCAGCCCGGATCGAGCGTGGCGCGACCGCTGGCGTGGTACGGGGGCTCG	171
QY	21	GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuValValGly	40
DB	172	GGGGGATCGCGCGCGCTGGCGCGGCTGGTCCAGCGGACTGAAGTGGTGGGC	231
QY	41	CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr	60
DB	232	TGCGCCCGCATGTGGGCAATCATCAGAGGTGGTGTGAATGTAAAGTGCAGGCTAC	291
QY	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
DB	292	CCCGGACTTTGATCCCTACAGATGTACCTATCAATGAAGAGCATCTCTCCATG	351
QY	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu	100
DB	352	TTCTCAGTATCCGTTCTCAGCACAGCGTGTAGACATCTGCATCAACAATGCTGGCTG	411
QY	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal	120
DB	412	GCCCGGCTGACACCTCTCTCAGCGACACCGTGGTGAAGAGCATGTTCAATGTG	471
QY	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
DB	472	AACGTGTGCGCTCAGCATCTGCACCGGAAGCTTACCAGTCCATGAAGGAGCGAAT	531
QY	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
DB	532	GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATCCCTG	591
QY	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
DB	592	TCTGTGACCCACTCTATAGTCCACCAAGTATGCCGTCATGCGCTGACAGAGGACTG	651
QY	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
DB	652	AGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGTGTG	711
QY	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr	220
DB	712	GTGGAGACACAATTGCGCTTCAAACTCCACGACAGGACCCCTGAGAGGCGAGCTGCCAC	771
QY	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240
DB	772	TATGAGCAATGAAGTGTCTCAACCCGAGGATGGCCGAGGCTGTTATCTACGTCCTC	831
QY	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260
DB	832	AGCACCCCGCACATCATCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGACC	891

RESULT 4	
ABS/4441	
ID	ABS74441 standard; cDNA; 1505 BP.
XX	AC ABS74441;
XX	DT 10-DEC-2002 (first entry)
XX	DE Human cDNA encoding secreted/transmembrane protein PRO1774.
KW	Human; ss; Gene; secreted protein; transmembrane protein; antirheumatic;
KW	antiarthritic; osteopathic; sports-related joint problem;
KW	articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX	Homo sapiens.
OS	US2002119130-A1.
XX	29-AUG-2002.
XX	06-DEC-2001; 2001US-00006867.
PR	29-OCT-1997; 97US-0063435P.
PR	29-OCT-1997; 97US-0064215P.
PR	22-APR-1998; 98US-0082737P.
PR	29-APR-1998; 98US-0083495P.
PR	15-MAY-1998; 98US-0085579P.
PR	02-JUN-1998; 98US-0087759P.
PR	04-JUN-1998; 98US-0088021P.
PR	04-JUN-1998; 98US-0088029P.
PR	04-JUN-1998; 98US-0088030P.
PR	10-JUN-1998; 98US-0088734P.
PR	10-JUN-1998; 98US-0088740P.
PR	10-JUN-1998; 98US-0088811P.
PR	10-JUN-1998; 98US-0088824P.
PR	10-JUN-1998; 98US-0088832P.
PR	11-JUN-1998; 98US-0088863P.
PR	12-JUN-1998; 98US-0089105P.
PR	16-JUN-1998; 98US-0089514P.
PR	17-JUN-1998; 98US-0089653P.
PR	19-JUN-1998; 98US-0089952P.
PR	22-JUN-1998; 98US-0090246P.
PR	24-JUN-1998; 98US-0090444P.
PR	25-JUN-1998; 98US-0090688P.
PR	25-JUN-1998; 98US-0090696P.
PR	26-JUN-1998; 98US-0090862P.
PR	02-JUL-1998; 98US-0091628P.
PR	10-AUG-1998; 98US-0096012P.
PR	17-AUG-1998; 98US-0096757P.
PR	18-AUG-1998; 98US-0096949P.
PR	18-AUG-1998; 98US-0096959P.
PR	26-AUG-1998; 98US-0097954P.
PR	26-AUG-1998; 98US-0097971P.
PR	01-SEP-1998; 98US-0097979P.
PR	01-SEP-1998; 98US-0098749P.
PR	10-SEP-1998; 98US-0099741P.
PR	10-SEP-1998; 98US-0099763P.
PR	10-SEP-1998; 98US-0099792P.
PR	10-SEP-1998; 98US-0099812P.
PR	10-SEP-1998; 98US-0099815P.
PR	16-SEP-1998; 98US-0100627P.
PR	16-SEP-1998; 98US-0100662P.
PR	16-SEP-1998; 98US-0100683P.
PR	17-SEP-1998; 98US-0100684P.
PR	17-SEP-1998; 98US-0100930P.
PR	22-SEP-1998; 98US-0101279P.
PR	23-SEP-1998; 98US-0101475P.
PR	24-SEP-1998; 98US-0101738P.
PR	24-SEP-1998; 98US-0101743P.
PR	24-SEP-1998; 98US-0101916P.
PR	30-SEP-1998; 98US-0102570P.

PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021030.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US0310720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

XX (GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

DR WPI; 2002-731348/79.
 DR P-PSDB; ABG95914.

PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 2; Fig 127; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95914-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5901
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid

CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the
 CC invention

XX SQ Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.35e-128	Length:	1505
Score:	1337.00	Matches:	260
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-063-735-128 (1-260) x ABS74441 (1-1505)

Qy	1	MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer	20
Db	112	ATGCCAGCGCCGCGCATGGAGCGGTGGCGCCGCCGCTGGCGCTGGTACGGGGCCCTCG	171
Qy	21	GlyGlyIleGlyAlaAlaValAlaAraAlaLeuValGlnGlnGlyLeuLysValValGly	40
Db	172	GGGGGCATCGCGCGCGCGTGGCCCGGCGCTGGTCCAGCAGGACTGAGGTGGTGGGC	231
Qy	41	CysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyr	60
Db	232	TGCGCCCGCATCTGTGGCAACATCGAGGAGTGGCTGTAATTAAGAGTGCAGGCTAC	291
Qy	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
Db	292	CCGGGAGCTTGTATCCCTTACAGATGTACCTATCAATGAAGAGGACATCCTCTCCATG	351
Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu	100
Db	352	TTCTCACTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG	411
Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal	120
Db	412	GCCCGGCTGACACCCCTGCTCTCAGGAGCAGCAGCAGTGGTGGAGGACATGTTCAATGTG	471
Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
Db	472	AACGTGCTGGCCCTCAGCATCTGCACAGGAGCCCTACCAGTCCATGAAGAGGCGGAAT	531
Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
Db	532	GTGGACATGGGCACATCATTAACATCAATAGCATGTCTGCCACCGAGTGTACCCCTG	591
Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
Db	592	TCGTGTACCCACTTCTATAGTGCACCAAGTATGCGCTCACTGCGCTGACAGAGGACTG	651
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
Db	652	AGGCAAGAGCTTCGGAGAGGCCACACCCATCCGAGCCACGTCGTCATCTCCAGGGTGTG	711
Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr	220
Db	712	GTGGAGACACAATTCCGCTTCAACTCCACGACAGAGCCCTGAGAGGAGGAGTGCACC	771
Qy	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240
Db	772	TATGAGCAATGAATGTCTCTCAACCCGAGGATGTGGCCGAGGCTGTATTCTACGTCCTC	831
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260

PR	17-AUG-1998;	98US-0096757P.	Qy	21	GlyGlyIleGlyAlaAlaValArgAlaLeuValGlnGlnGlyLeuLysValValGly	40
PR	17-AUG-1998;	98US-0096766P.	Db	172	GGGGGCATCGCGCGCGCTGGCCCGGGCCCTGGTCCAGCAGGACTGAAGAGTGGTGGC	231
PR	17-AUG-1998;	98US-0096867P.	Qy	41	CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr	60
PR	18-AUG-1998;	98US-0096897P.	Db	232	TGCGCCCGCAGTGTGGGCAACATCGAGGAGCTGGCTGCTGATGTAGAGTGCAGGTAC	291
PR	18-AUG-1998;	98US-0096959P.	Qy	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
PR	26-AUG-1998;	98US-0097952P.	Db	292	CCCGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATG	351
PR	26-AUG-1998;	98US-0097954P.	Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100
PR	26-AUG-1998;	98US-0097971P.	Db	352	TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG	411
PR	02-SEP-1998;	98US-0098723P.	Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal	120
PR	02-SEP-1998;	98US-0098803P.	Db	412	GCCCGGCTGACACCCCTGCTCTCAGGCAGCACCAAGTGGTTGGAAGGACATGTTCAATGTG	471
PR	02-SEP-1998;	98US-0098821P.	Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
PR	09-SEP-1998;	98US-0098843P.	Db	472	AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCACTCCATGAAGGAGCGAAT	531
PR	10-SEP-1998;	98US-0099602P.	Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
PR	10-SEP-1998;	98US-0099741P.	Db	532	GTGGACGATGGGCACATCATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTG	591
PR	15-SEP-1998;	98US-0100388P.	Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
PR	16-SEP-1998;	98US-0100662P.	Db	592	TCTGTGACCACCTCTATAGTGCACCAAGTATGCCCTCACTGGCTGACAGAGGACTG	651
PR	16-SEP-1998;	98US-0100684P.	Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
PR	16-SEP-1998;	98US-0101751P.	Db	652	AGGCAGAGCTTCGGGAGGCCACACCCACATCCGAGCCACGTCATCTCTCCAGGTGTG	711
PR	23-SEP-1998;	98US-0101471P.	Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr	220
PR	23-SEP-1998;	98US-0101472P.	Db	712	GTGGAGACACAATTGCGCTTCAAACTCCACGACAGGACCCCTGAGAAAGGAGCTGCCACC	771
PR	23-SEP-1998;	98US-0101475P.	Qy	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240
PR	24-SEP-1998;	98US-0101738P.	Db	772	TATGAGCAATGAAGTGTCTCAAAACCCGAGAGTGTGCCGAGGCTGTTATCTAGTCTC	831
PR	24-SEP-1998;	98US-0101743P.	Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260
PR	25-SEP-1998;	98US-0101766P.	Db	832	AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACC	891
PR	29-SEP-1998;	98US-0102207P.	RESULT 6			
PR	29-SEP-1998;	98US-0102240P.	ACA75688			
PR	29-SEP-1998;	98US-0102330P.	ID	ACA75688	standard; cDNA; 1505 BP.	
PR	29-SEP-1998;	98US-0102331P.	XX	ACA75688;		
PR	30-SEP-1998;	98US-0102487P.	XX	07-JUL-2003	(first entry)	
PR	30-SEP-1998;	98US-0102570P.	DT	Novel human secreted and transmembrane protein PRO1774	cDNA.	
PR	30-SEP-1998;	98US-0102571P.	DE	Human; secreted and transmembrane protein: PRO; gene therapy;		
PR	01-OCT-1998;	98US-0102684P.	KW	tumour necrosis factor-alpha release; TNF-alpha release;		
PR	02-OCT-1998;	98US-0102687P.	KW	chondrocyte proliferation; chondrocyte differentiation; tumour;		
PR	06-OCT-1998;	98US-0102965P.	KW	adrenal tumour; lung tumour; colon tumour; breast tumour;		
PR	06-OCT-1998;	98US-0103258P.	XX	prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.		
PR	06-OCT-1998;	98US-0103449P.	OS	Homo sapiens.		
PR	07-OCT-1998;	98US-00168978.	XX	US2003032127-A1.		
PR			PN	13-FEB-2003.		
PR			XX	26-JUN-2002;	2002US-00183012.	
PR			PF	18-SEP-1997;	97US-0059263P.	
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PR			PR			

Alignment Scores:
 Pred. No.: 2,35e-128
 Score: 1337.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 7
 Gaps: 0

US-10-063-735-128 (1-260) x ABX78716 (1-1505)

Qy 1 MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
 Db 112 ATGCCAGCCCGCATGGAGCGTGGCGCAGCCGCTGGCTGGTGAAGCGGGGCTCG 171

PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 28-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066468P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
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PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
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PR 24-JUN-1998; 98US-0090429P.
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PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
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PR 01-JUL-1998; 98US-0091359P.
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PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 17-AUG-1998; 98US-0096757P.
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PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
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PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
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PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.

QY	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
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PR	23-SEP-1998;	98US-0101477P.
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PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	30-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
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PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.

Alignment Scores:

Pred. No.:	2,35e-128	Length:	1505
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-063-735-128 (1-260) x ACA75688 (1-1505)

QY	1	MetalArgProGlyWecGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer	20
Db	112	ATGCCAGCCCGGCATGGAGCGGTGGCGCACCGGCTGGCGTGGTACGGGGGCGCTCG	171
QY	21	GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuIysValValGly	40
Db	172	GGGGGCATCGCGCGCGCGCTGGCCCGGGCCCTGGTCCACAGGGACTGAAGTGTGGGCG	231
QY	41	CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysIysSerAlaGlyTyr	60
Db	232	TGCGCCCGCACTGTGGGCAACATCGAGGAGCTGGCTGCTGANTGTAAGAGTCGACGGCTAC	291
QY	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
Db	292	CCCGGGACTTTGATCCCTTACAGATGTGACCTTATCAAAATGAAGAGACATCCTCTCCATG	351
QY	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100
Db	352	TTCTCAGCTATCCGTTCTCAGCACAGCGGTGAGACATCTGCATCAACAATGCTGGCTTG	411
QY	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpIysAspMetPheAsnVal	120
Db	412	GCCCGGCTGACACCTGCTCTCAGCAGCACCAGTGGTGGAGGACATGTTCAATGTG	471
QY	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetIysGluArgAsn	140
Db	472	AACGTGTGGCCCTCAGCATCTGCACAGGGAAGCCTACCACTCCATGAAGAGCGGAAT	531
QY	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValIleuProLeu	160
Db	532	GTGACCATGGGCATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG	591

PR	01-APR-1998;	98US-0080327P.	PR	25-JUN-1998;	98US-0090690P.
PR	01-APR-1998;	98US-0080333P.	PR	25-JUN-1998;	98US-0090694P.
PR	08-APR-1998;	98US-0081049P.	PR	25-JUN-1998;	98US-0090695P.
PR	08-APR-1998;	98US-0081070P.	PR	25-JUN-1998;	98US-0090696P.
PR	09-APR-1998;	98US-00811195P.	PR	26-JUN-1998;	98US-00105413.
PR	15-APR-1998;	98US-0081838P.	PR	26-JUN-1998;	98US-0090862P.
PR	21-APR-1998;	98US-0082568P.	PR	26-JUN-1998;	98US-0090863P.
PR	21-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0091010P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-0091359P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-0091544P.
PR	28-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-0091478P.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0091486P.
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PR	06-MAY-1998;	98US-0084414P.	PR	04-AUG-1998;	98US-0095282P.
PR	07-MAY-1998;	98US-0084639P.	PR	10-AUG-1998;	98US-0095988P.
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PR	07-MAY-1998;	98US-0084643P.	PR	17-AUG-1998;	98US-0096757P.
PR	15-MAY-1998;	98US-0085579P.	PR	17-AUG-1998;	98US-0096766P.
PR	15-MAY-1998;	98US-0085580P.	PR	17-AUG-1998;	98US-0096867P.
PR	15-MAY-1998;	98US-0085582P.	PR	17-AUG-1998;	98US-0096891P.
PR	15-MAY-1998;	98US-0085700P.	PR	17-AUG-1998;	98US-0096897P.
PR	18-MAY-1998;	98US-0086023P.	PR	18-AUG-1998;	98US-0096949P.
PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0096959P.
PR	22-MAY-1998;	98US-0086486P.	PR	26-AUG-1998;	98US-0097022P.
PR	28-MAY-1998;	98US-0087098P.	PR	26-AUG-1998;	98US-0097952P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097954P.
PR	02-JUN-1998;	98US-0087609P.	PR	26-AUG-1998;	98US-0097955P.
PR	02-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-0097971P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097974P.
PR	04-JUN-1998;	98US-0088025P.	PR	26-AUG-1998;	98US-0098014P.
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PR	04-JUN-1998;	98US-0088326P.	PR	02-SEP-1998;	98US-0098803P.
PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-0098821P.
PR	05-JUN-1998;	98US-0088202P.	PR	02-SEP-1998;	98US-0098843P.
PR	05-JUN-1998;	98US-0088211P.	PR	09-SEP-1998;	98US-0099602P.
PR	05-JUN-1998;	98US-0088217P.	PR	10-SEP-1998;	98US-0099741P.
PR	09-JUN-1998;	98US-0088655P.	PR	10-SEP-1998;	98US-0099754P.
PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088738P.	PR	15-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088824P.	PR	16-SEP-1998;	98US-0100664P.
PR	10-JUN-1998;	98US-0088825P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088826P.	PR	16-SEP-1998;	98US-0100683P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100919P.
PR	11-JUN-1998;	98US-0088867P.	PR	17-SEP-1998;	98US-0100930P.
PR	12-JUN-1998;	98US-0089090P.	PR	18-SEP-1998;	98US-0100849P.
PR	12-JUN-1998;	98US-0089105P.	PR	18-SEP-1998;	98US-0101014P.
PR	16-JUN-1998;	98US-0089511P.	PR	18-SEP-1998;	98US-0101068P.
PR	16-JUN-1998;	98US-0089514P.	PR	23-SEP-1998;	98US-0101471P.
PR	17-JUN-1998;	98US-0089538P.	PR	23-SEP-1998;	98US-0101472P.
PR	17-JUN-1998;	98US-0089598P.	PR	23-SEP-1998;	98US-0101475P.
PR	17-JUN-1998;	98US-0089653P.	PR	23-SEP-1998;	98US-0101477P.
PR	18-JUN-1998;	98US-0089908P.	PR	24-SEP-1998;	98US-0101738P.
PR	19-JUN-1998;	98US-0089952P.	PR	24-SEP-1998;	98US-0101739P.
PR	22-JUN-1998;	98US-0090246P.	PR	24-SEP-1998;	98US-0101743P.
PR	22-JUN-1998;	98US-0090252P.	PR	25-SEP-1998;	98US-0101922P.
PR	22-JUN-1998;	98US-0090254P.	PR	25-SEP-1998;	98US-0101786P.
PR	24-JUN-1998;	98US-0090423P.	PR	29-SEP-1998;	98US-0102207P.
PR	24-JUN-1998;	98US-0090435P.	PR	29-SEP-1998;	98US-0102240P.
PR	24-JUN-1998;	98US-0090444P.	PR	29-SEP-1998;	98US-0102330P.
PR	24-JUN-1998;	98US-0090461P.	PR	29-SEP-1998;	98US-0102331P.
PR	24-JUN-1998;	98US-0090535P.	PR	30-SEP-1998;	98US-0102487P.
PR	24-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102570P.
PR	25-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090678P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102687P.

PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-00168978.

Alignment Scores:

Pred. No.: 2,35e-128 Length: 1505
 Score: 1337.00 Matches: 260
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-063-735-128 (1-260) x ACA71168 (1-1505)

QY 1 MetalAArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
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 QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
 Db 172 GGGGCGATCGGCGCGCGCTGGCGCGGCGCTGGCTGGCGAGGAGACTGAAGGTGGTGGC 231
 QY 41 CysAlaArgThrValGlyAsnIleGluLeuAlaGluCysLysSerAlaGlyTyr 60
 Db 232 TCGCGCCGCACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGTAC 291
 QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMet 80
 Db 292 CCCGGGACTTTGATCCCCCTCAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
 QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
 Db 352 TTCTCAGTATCCGTTCTCAGCAGCGGTGAGACATCTGCATCAACAATGCTGGCTTG 411
 QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
 Db 412 GCCCGGCTGACACCTCTCTCAGGAGCACCAGTGGTGGAGGACATGTTCAATGTG 471
 QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
 Db 472 AACGTGTCGGCCCTCAGCATCTGACACAGGAGCCTACCAAGTCCATGAAGAGCGGAAT 531
 QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
 Db 532 GTGGACGNTGGCACAATCATTAATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
 QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
 Db 592 TCTGTGACCCACTTCTATAGTCCACCAAGTATGCCGTCACTGGCTGACAGAGGACTG 651
 QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
 Db 652 AGGCAAGAGCTTCGGAGGCGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTG 711
 QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
 Db 712 GTGGAGACAAATTCGCTTCAAACTCCACGACGAGGACCTGAGAGGAGGCTGCCACC 771
 QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
 Db 772 TATGAGCAATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTATCTAGTCTCTC 831
 QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
 Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCGCCCGAGGAGGTGACC 891

RESULT 8

ACC87696

ID ACC87696 standard; cDNA; 1505 BP.

XX

AC ACC87696;

XX

05-AUG-2003 (first entry)

Human secreted polypeptide PRO1774-encoding cDNA, SEQ ID NO:377.

Human; PRO; secreted protein; transmembrane protein;
 extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 chondrocyte; proliferation; differentiation; cartilage disorder;
 bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 adrenal tumour; lung; colon; breast; prostate; kidney; cervix;
 liver; drug screening; transgenic animal; genetic analysis;
 antiarthritic; vulnerary; gene therapy; gene; ss.

Homo sapiens.

US2003027278-A1.

06-FEB-2003.

21-JUN-2002; 2002US-00176987.

18-SEP-1997; 97US-0059263P.
 18-SEP-1997; 97US-0059266P.
 17-OCT-1997; 97US-0062250P.
 21-OCT-1997; 97US-0063486P.
 24-OCT-1997; 97US-0063130P.
 24-OCT-1997; 97US-0063112P.
 28-OCT-1997; 97US-0063540P.
 28-OCT-1997; 97US-0063541P.
 28-OCT-1997; 97US-0063544P.
 28-OCT-1997; 97US-0063546P.
 29-OCT-1997; 97US-0063734P.
 31-OCT-1997; 97US-0063870P.
 31-OCT-1997; 97US-0064103P.
 13-NOV-1997; 97US-0065311P.
 21-NOV-1997; 97US-0066120P.
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 24-NOV-1997; 97US-0066772P.
 11-DEC-1997; 97US-0069335P.
 12-DEC-1997; 97US-0069425P.
 17-DEC-1997; 97US-0069870P.
 18-DEC-1997; 97US-0068017P.
 10-MAR-1998; 98US-0077450P.
 11-MAR-1998; 98US-0077632P.
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 20-MAR-1998; 98US-0078886P.
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 31-MAR-1998; 98US-0080194P.
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 08-APR-1998; 98US-0081049P.
 08-APR-1998; 98US-0081070P.
 09-APR-1998; 98US-0081195P.
 15-APR-1998; 98US-0081838P.
 21-APR-1998; 98US-0082568P.
 21-APR-1998; 98US-0082569P.
 22-APR-1998; 98US-0082704P.
 22-APR-1998; 98US-0082797P.
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 06-MAY-1998; 98US-0084414P.
 07-MAY-1998; 98US-0084639P.
 07-MAY-1998; 98US-0084640P.
 07-MAY-1998; 98US-0084643P.
 15-MAY-1998; 98US-0085579P.
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 15-MAY-1998; 98US-0085582P.

DT

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QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMet 80
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 QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
 Db 352 TTCTCAGCTATCCGTTCTCAGCACAGCGGTAGACATCTGCATCAACAATGCTGGCTG 411
 QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrPheAsnVal 120
 Db 412 GCCCGGCTGACACCTGCTCTCAGCAGCACCATGTTGGAAGGACATGTTCAATGTG 471
 QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
 Db 472 AAGGTGCTGGCCCTCAGCATCTGCACACGGGAGCTTACAGTCCATGAAGAGCGGAAT 531
 QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
 Db 532 GTGGACGATGGGCACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
 QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
 Db 592 TCTGTACCCACTTCTTAGTGCCACCAAGATGTCCTGCTGCTGCTGCTGCTGCTGCTG 651
 QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
 Db 652 AGGCAAGAGCTTCGGGAGGCCACACACATCCAGCAGCGTGCATCTCTCCAGGTGTG 711
 QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
 Db 712 GTGGAGACACAAATTCGCTTCAAACTCCACGACAGGACCTGAGAGGCGAGTGCACACC 771
 QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
 Db 772 TATGAGCAATGAAGTGTCTCAAACTCCAGGATGTCGCGAGGTGTATCTACGTCCTC 831
 QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
 Db 832 AGCACCCCGCACATCCAGATGGAGACATCCAGATGAGGCGCCACGAGCAGGTGACC 891
 RESULT 9
 ACC87082
 ID ACC87082 standard; cDNA; 1505 BP.
 AC ACC87082;
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 XX
 DT 05-AUG-2003 (first entry)
 DE Human secreted polypeptide PRO1774-encoding cDNA, SEQ ID NO:377.
 KW Human; PRO; secreted protein; transmembrane protein;
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antiarthritic; vulnery; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX US2003036159-A1.
 XX
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 PD 20-FEB-2003.
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 PF 02-JUL-2002; 2002US-00188773.
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 PR 28-OCT-1997; 97US-0063540P.
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 PR 22-APR-1998; 98US-0082704P.
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DT 09-AUG-2003 (first entry)
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KW Human; Gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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XX 27-JUN-2003 (first entry)

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XX chromosome mapping; gene mapping; cytostatic; gene therapy; gene, ss.
XX Homo sapiens.

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Gaps: 0
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US-10-063-735-128 (1-260) x ACC89538 (1-1505)

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Qy	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80	PR	24-OCT-1997;	97US-0063121P.
Db	292	CCCGGACTTTGATCCCTCAGATGTGACCTATCAATGAAGAGCATCTCTCCATG	351	PR	28-OCT-1997;	97US-0063540P.
Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100	PR	28-OCT-1997;	97US-0063541P.
Db	352	TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTG	411	PR	28-OCT-1997;	97US-0063544P.
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Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140	PR	13-NOV-1997;	97US-0065311P.
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Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160	PR	24-NOV-1997;	97US-0066466P.
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Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180	PR	11-DEC-1997;	97US-0069335P.
Db	592	TCTGTGACCCACTTCTATAGTGCCACCAAGATGCGCTCATGCGCTCAGAGAGGACTG	651	PR	17-DEC-1997;	97US-0069870P.
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200	PR	18-DEC-1997;	97US-0068017P.
Db	652	AGCAAGAGCTTCGGAGGCGCCAGACCACCATCCGAGCCAGTGCATCTCTCCAGGTGTG	711	PR	10-MAR-1998;	98US-0077450P.
Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr	220	PR	11-MAR-1998;	98US-0077632P.
Db	712	GTGGAGACACAATTCGCCTTCAAACTCCACACAGGACCCCTGAGAGGCGAGCTGCCACC	771	PR	20-MAR-1998;	98US-0078886P.
Qy	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240	PR	20-MAR-1998;	98US-0078939P.
Db	772	TATGAGCAAAATGAAGTGTCTAAACCCGAGGATGTGGCCGAGCTGTTATCTACGTCCTC	831	PR	27-MAR-1998;	98US-0079664P.
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260	PR	31-MAR-1998;	98US-0080107P.
Db	832	AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACC	891	PR	31-MAR-1998;	98US-0080194P.

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DT 25-JUL-2003 (first entry)
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KW Human; secreted and transmembrane protein; PRO; transgenic animal;
KW knockout; chromosome identification; tissue typing; tumour;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumor necrosis factor-alpha release stimulator; gene; ss.
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XX
PN US2003036144-A1.
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PD 20-FEB-2003.
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PF 01-JUL-2002; 2002US-00187601.

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 KW tumour necrosis factor-alpha; gene therapy.
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Db 652 AGGCAAGAGCTTCGGGAGGCCACACCATCCGAGCCACGTGCATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
Db 712 GTGGAGACAAATTCGCTTCAACTCCACGACAAAGGACCTGAGAAGCGAGCTGCCACC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTTATCTACGTCTC 831
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGATCCAGATGAGGCCACCGGAGAGGTGACC 891
```


GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 16:36:27 : Search time 422 Seconds

(without alignments)

3109.801 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence:

1 MARPGMRWRDLALVTGAS.....STPAHIQIGIQMRPTQV 260

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastp -SUFFIX=rnnp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10063735@cgn_1_783@runat_15092004_103012_8512
-NCFU=6 -ICPU=3 -NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=130 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
------------	-------	-------	--------	----	----	-------------

1	1337	100.0	1493	10	US-09-971-392-222	Sequence 222, App
2	1337	100.0	1505	13	US-10-206-915-377	Sequence 377, App
3	1337	100.0	1505	13	US-10-199-670-377	Sequence 377, App
4	1337	100.0	1505	13	US-10-201-858-377	Sequence 377, App
5	1337	100.0	1505	13	US-10-205-890-377	Sequence 377, App
6	1337	100.0	1505	13	US-10-208-024-377	Sequence 377, App
7	1337	100.0	1505	13	US-10-201-853-377	Sequence 377, App
8	1337	100.0	1505	13	US-10-063-745-127	Sequence 127, App
9	1337	100.0	1505	13	US-10-063-512-127	Sequence 127, App
10	1337	100.0	1505	13	US-10-063-513-127	Sequence 127, App
11	1337	100.0	1505	13	US-10-063-569-127	Sequence 127, App
12	1337	100.0	1505	13	US-10-063-551-127	Sequence 127, App
13	1337	100.0	1505	13	US-10-174-581-377	Sequence 377, App
14	1337	100.0	1505	13	US-10-176-483-377	Sequence 377, App
15	1337	100.0	1505	13	US-10-176-749-377	Sequence 377, App
16	1337	100.0	1505	13	US-10-176-914-377	Sequence 377, App
17	1337	100.0	1505	13	US-10-176-915-377	Sequence 377, App
18	1337	100.0	1505	13	US-10-063-555-127	Sequence 127, App
19	1337	100.0	1505	13	US-10-063-563-127	Sequence 127, App
20	1337	100.0	1505	13	US-10-063-594-127	Sequence 127, App
21	1337	100.0	1505	13	US-10-063-553-127	Sequence 127, App
22	1337	100.0	1505	13	US-10-063-554-127	Sequence 127, App
23	1337	100.0	1505	13	US-10-176-484-377	Sequence 377, App
24	1337	100.0	1505	13	US-10-180-550-377	Sequence 377, App
25	1337	100.0	1505	13	US-10-183-014-377	Sequence 377, App
26	1337	100.0	1505	13	US-10-187-738-377	Sequence 377, App
27	1337	100.0	1505	13	US-10-187-740-377	Sequence 377, App
28	1337	100.0	1505	13	US-10-187-883-377	Sequence 377, App
29	1337	100.0	1505	13	US-10-194-363-377	Sequence 377, App
30	1337	100.0	1505	13	US-10-194-460-377	Sequence 377, App
31	1337	100.0	1505	13	US-10-194-463-377	Sequence 377, App
32	1337	100.0	1505	13	US-10-194-484-377	Sequence 377, App
33	1337	100.0	1505	13	US-10-195-884-377	Sequence 377, App
34	1337	100.0	1505	13	US-10-195-896-377	Sequence 377, App
35	1337	100.0	1505	13	US-10-196-744-377	Sequence 377, App
36	1337	100.0	1505	13	US-10-196-755-377	Sequence 377, App
37	1337	100.0	1505	13	US-10-196-757-377	Sequence 377, App
38	1337	100.0	1505	13	US-10-197-704-377	Sequence 377, App
39	1337	100.0	1505	13	US-10-197-710-377	Sequence 377, App
40	1337	100.0	1505	13	US-10-198-758-377	Sequence 377, App
41	1337	100.0	1505	13	US-10-198-766-377	Sequence 377, App
42	1337	100.0	1505	13	US-10-199-304-377	Sequence 377, App
43	1337	100.0	1505	13	US-10-199-309-377	Sequence 377, App
44	1337	100.0	1505	13	US-10-199-313-377	Sequence 377, App
45	1337	100.0	1505	13	US-10-199-456-377	Sequence 377, App

ALIGNMENTS

RESULT 1

US-09-971-392-222
; Sequence 222, Application US/099711392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Pearson, David P.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 222
; LENGTH: 1493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 422389.9

US-09-971-392-222

Alignment Scores:

Pred. No.: 1.81e-165 Length: 1493
 Score: 1337.00 Matches: 260
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-063-735-128 (1-260) x US-09-971-392-222 (1-1493)

Qy 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
 Db 112 ATGCCAGCGCCGCGCATGGAGCGGTGGCGCGACCGGCTGGTACCGGGGCGCTCG 171
 Qy 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLeuValValGly 40
 Db 172 GGGGCGATCGCGCGCGCGCTGGCGCGCGCTGGTCCAGCAGGAGTGAAGTGGTGGGC 231
 Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
 Db 232 TGGCGCCGCACTGTGGGCAACATCGAGGAGTGGTCTGAATGTAAAGTGCAGGCTAC 291
 Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleSerMet 80
 Db 292 CCGGGGACTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
 Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
 Db 352 TTCTCAGCTATCCGTTCTTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
 Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
 Db 412 GCGCGCGCTGACACCGCTGCTTCAGCGAGCAGTGGTGGTGAAGAGGACATGTTCAATGTG 471
 Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
 Db 472 AACGTCGTGGCGCTCAGCATCTGCACACGGGAAGCTTACCATGTCATGAAGAGCGGAAT 531
 Qy 141 ValAspAspGlyHisIleAlaIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
 Db 532 GTGGAGCATGGGCATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATCCCTCG 591
 Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
 Db 592 TCTGTGACCCACTTCTATAGTGCCCAAGTATGCGTCACTGCGCTGACAGAGGAGCTG 651
 Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
 Db 652 AGGCNAGAGCTTCGGGAGCGCCAGACCCACATCCAGGCGCATCTCTCCAGGTGTG 711
 Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
 Db 712 GTGGAGACACAATTCGCTTCAACTCCACGACAGGAGCCCTGTGAAGAGGAGTCCACC 771
 Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
 Db 772 TATGAGCAATAGAGTGTCTCAACCCGAGGATGTGGCGGAGGCTGTATCTACGCTCCTC 831
 Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
 Db 832 AGACCCCGGCACATTCAGATTGGAGACATCCAGATGAGGCCCCAGGAGCGAGGTGACC 891

RESULT 2

US-10-206-915-377
 ; Sequence 377, Application US/10206915
 ; Publication No. US20040029221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zenin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P34301C513
 ; CURRENT APPLICATION NUMBER: US/10/206,915
 ; CURRENT FILING DATE: 2002-07-26
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 377
 ; LENGTH: 1505
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-206-915-377

Alignment Scores:

Pred. No.: 1.83e-165 Length: 1505
 Score: 1337.00 Matches: 260
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-206-915-377 (1-1505)

Qy 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
 Db 112 ATGCCAGCGCCGCGCATGGAGCGGTGGCGCGACCGGCTGGTACCGGGGCGCTCG 171
 Qy 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
 Db 172 GGGGCGATCGCGCGCGCGCTGGCGCGCGCTGGTCCAGCAGGAGTGAAGTGGTGGGC 231
 Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
 Db 232 TGGCGCCGCACTGTGGGCAACATCGAGGAGTGGTCTGAATGTAAAGTGCAGGCTAC 291
 Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleSerMet 80
 Db 292 CCGGGGACTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
 Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
 Db 352 TTCTCAGCTATCCGTTCTTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
 Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
 Db 412 GCGCGCGCTGACACCGCTGCTCTCAGCGAGCAGTGGTGGTGAAGAGGACATGTTCAATGTG 471

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QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AAGTGTGTCCTCCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGGAGCGAAT 531
QY 141 ValAspAspGlyHisIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCACCAAGTATGCGCTCACTGCGCTGCACAGAGGACTG 651
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGTCTCGGAGGGCCACACCCACATCCGAGCCACGTCATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
Db 712 GTGAGACACAAATTCGCTTCAAACTCCACGACAGGACCTGAGAGGCGAGTGCACCC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTATCTACGTCCTC 831
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCGCCAGGAGCGGTGACC 891

RESULT 3
US-10-199-670-377
; Sequence 377, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
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; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-670-377

Alignment Scores:
Pred. No.: 1,83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-199-670-377 (1-1505)
QY 1 MetAlaArgProGlyMetGluArgTTPArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCCCGCATGGAGCGGTGGCGGACCCGGCTGGCTGTGACGGGGGCGCTCG 171
QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCCGCACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGACGGCTAC 291
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCGTCTTCAGCACGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
Db 412 GCCCGGCTGACACCCCTGCTCTCAGGCAGCACCCAGTGGTGGAGGAGACATGTTCAATGTG 471
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGAGCGGAAT 531
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCACCAAGTATGCGCTCACTGGCTGCACAGAGGACTG 651
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGCTTCGGAGGCGCCAGACCCACATCCGAGCCACGTCGATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
Db 712 GTGGAGACACAAATTCGCTTCAAACTCCACGACAGGACCTGAGAGGCGAGTGCACCC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTATCTACGTCCTC 831
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCGCCAGGAGCGGTGACC 891

RESULT 4
US-10-858-377
; Sequence 377, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
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:	APPLICANT:	Chen,Jian
:	APPLICANT:	Desnoyers,Luc
:	APPLICANT:	Goddard,Audrey
:	APPLICANT:	Godowski,Paul J.
:	APPLICANT:	Gurney,Austin L.
:	APPLICANT:	Pan,James
:	APPLICANT:	Smith,Victoria
:	APPLICANT:	Watanabe,Colin K.
:	APPLICANT:	Wood,William I.
:	APPLICANT:	Zhang,Zemin
:	TITLE OF INVENTION:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
:	FILE REFERENCE:	P3430RIC464
:	CURRENT APPLICATION NUMBER:	US/10/201,858
:	CURRENT FILING DATE:	2002-07-23
:	PRIOR APPLICATION NUMBER:	10/052586
:	PRIOR FILING DATE:	2002-01-15
:	PRIOR APPLICATION NUMBER:	60/059263
:	PRIOR FILING DATE:	1997-09-18
:	PRIOR APPLICATION NUMBER:	60/059266
:	PRIOR FILING DATE:	1997-09-18
:	PRIOR APPLICATION NUMBER:	60/062250
:	PRIOR FILING DATE:	1997-10-17
:	PRIOR APPLICATION NUMBER:	60/063120
:	PRIOR FILING DATE:	1997-10-24
:	PRIOR APPLICATION NUMBER:	60/063121
:	PRIOR FILING DATE:	1997-10-24
:	PRIOR APPLICATION NUMBER:	60/063486
:	PRIOR FILING DATE:	1997-10-21
:	PRIOR APPLICATION NUMBER:	60/063540
:	PRIOR FILING DATE:	1997-10-28
:	PRIOR APPLICATION NUMBER:	60/063541
:	PRIOR FILING DATE:	1997-10-28
:	PRIOR APPLICATION NUMBER:	60/063544
:	PRIOR FILING DATE:	1997-10-28
:	Prior Application data removed - See File Wrapper or PALM.	
:	NUMBER OF SEQ ID NOS:	612
:	SEQ ID NO 377	
:	LENGTH:	1505
:	TYPE:	DNA
:	ORGANISM:	Homo Sapien
:	US-10-201-858-377	
:	Alignment Scores:	
:	Pred. No.:	1-83e-165 Length: 1505
:	Score:	1337.00 Matches: 260
:	Percent Similarity:	100.00% Conservative: 0
:	Best Local Similarity:	100.00% Mismatches: 0
:	Query Match:	100.00% Indels: 0
:	DB:	13 Gaps: 0
:	US-10-063-735-128 (1-260) x US-10-201-858-377 (1-1505)	
:QY	1	MetaAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
:Db	112	ATGCCACAGCCCGCATGGATGAGCGGTGGCGGCACCCTGGTGGCTGGTGACCGGGGCTCG 171
:QY	21	GlyGVlledgIyAlaAlaValAlaAargAlaLeuValGlnGlnGlyLeuLysValValGly 40
:Db	172	GGGGGCATCGGGCGGCGCTGGCCCGGSCCTGTGTCAGCAGGGACTGAAGGTGGTGGGC 231
:QY	41	CysAlaAtgThrValGlyAsnIleGluGluAlaAlaGluCySLysSerAlaGlyTyr 60
:Db	232	TGGCCCGCACCTGTGGCAACATCAGAGAGCTGGCTCTGNATGTATAGAGTGGAGGCTAC 291
:QY	61	ProGlyThrLeuIleProTyrrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
:Db	292	CCGGGACATTGATCCCCCTACAGATGTGACCTATCAAATGAAGAGGACATCCTCTCCATG 351
:QY	81	PheSerAlaileArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
:Db	352	TTCTCAGCTATCCGHTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGCTTG 411

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 377

; LENGTH: 1505

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-205-890-377

Alignment Scores:

Pred. No.: 1,83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-205-890-377 (1-1505)

Qy 1 MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCCCGCATGGAGCGGTGGCGGACCGCGCTGGCGCTGGGTGACGGGGGCGCTCG 171
Qy 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCG 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCGCGCATGTGGGCAACATCGAGGAGTGGCTGCTGAATGAAGAGTGCAGGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCGGGGACTTGTATCCCTCAGATGTGACCTATCAATGAAGAGGACATCTCTCCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCGTTCTCAGCAGCGGGTGTAGACATCTGCATCAACATGCTGGCTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCCCGGCTGACACCTGCTCTCAGGCGACACAGTGGTGGAAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AAGTGTGCGCTTCAGCATCTGCACACGGAAGCCTACCATGCTCATGAAGGCGGAAT 531
Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGACCATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGCTCACTGCCGTGCACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGCTTCGGGAGGCCACAGCCACATCCGAGCCAGTGCATCTCTCCAGGTGTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
Db 712 GTGGAGACACAAATTCGCTTCAAACTCCACGACAAGGACCCCTGAGAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGTGTATCTACGCTCCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACATCTCAGATTTGGAGACATCCAGATGAGGCCCGCCACGGAGGTGACC 891

RESULT 6

US-10-208-024-377

; Sequence 377, Application US/10208024

; Publication No. US20040048335A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: F3430R1C538

; CURRENT APPLICATION NUMBER: US/10/208,024

; CURRENT FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 377

; LENGTH: 1505

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-208-024-377

Alignment Scores:

Pred. No.: 1,83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-208-024-377 (1-1505)

Qy 1 MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCCCGCATGGAGCGGTGGCGGACCGCGCTGGCGCTGGGTGACGGGGGCGCTCG 171
Qy 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCG 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCGCGCATGTGGGCAACATCGAGGAGTGGCTGCTGAATGAAGAGTGCAGGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCGGGGACTTGTATCCCTCAGATGTGACCTATCAATGAAGAGGACATCTCTCCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100

```
Db 352 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
Db 412 GCGCGGCTCAGACCCCTCTCTCAGGACAGCCAGTGTGTGGAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACCGGAAGCTACCACTCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGACGATGGCGCATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCCACCAAGATATGCCGTCACTGCGCTGACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGCTTCGGGAGGCCACACCATCCGAGGCGCATCTCTCCAGGTGTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
Db 712 GTGAGACACAAATTCGCTTCAAACTCCACGAAGGACCTGAGAAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCCGAGATGTGGCCAGGTGTTATCTACGTCCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACC 891
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RESULT 7

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US-10-201-853-377
; Sequence 377, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
```

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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-853-377
```

Alignment Scores:

Pred. No.:	1,83e-165	Length:	1505
Score:	1337.00	Matches:	260
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-063-735-128 (1-260) x US-10-201-853-377 (1-1505)

Qy	1	MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer	20
Db	112	ATGCCAGGCGCGCATGGAGCGGTGGCGACCGGCTGGCTGGTACGGGGGCGCTCG	171
Qy	21	GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly	40
Db	172	GGGGGCAATCGCGCGCGCGCTGGCCCGGCGCTGGTCCAGAGGAGCTGAAGGTGGTGGGC	231
Qy	41	CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr	60
Db	232	TGCGCCCGCATCTGGGCAACATCGAGAGCTGGCTGCTGAATGTAGAGTGCAGGCTAC	291
Qy	61	ProGlyThrIleuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
Db	292	CCCGGAGCTTTGATCCCGCTACAGATGTGACCTATAAATGAAGAGGACATCCTCTCCATG	351
Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100
Db	352	TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGGCTTG	411
Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal	120
Db	412	GCGCGGCTGACACCTGCTCTCAGGACAGCACCACTGGTGGAAAGGACATGTTCAATGTG	471
Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
Db	472	AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGAAGAGCGGAAT	531
Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
Db	532	GTGACGATGGCGCATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG	591
Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
Db	592	TCGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGACTG	651
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
Db	652	AGGCAAGAGCTTCGGGAGGCCACACCATCCGAGGACCTGAGAAGGCGAGTGTG	711
Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr	220
Db	712	GTGAGACACAAATTCGCTTCAAACTCCACGAAGGACCTGAGAAGGCGAGTGTG	771
Qy	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240
Db	772	TATGAGCAAAATGAAGTGTCTCAAAACCCGAGATGTGGCCAGGTGTTATCTACGTCCTC	831
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260
Db	832	AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACC	891


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RESULT 8
US-10-063-745-127
; Sequence 127, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-127

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-745-127 (1-1505)

Qy 1 MetAlaArgProGlyMetGluAtrGTPArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCGCGCATGGAGCGGTGGCGGACCGGCTGGCGCTGGAGCGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaValAlaAraGAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGGCGCGCGTGGCCCGGCGCTGGTCCAGCAGGAGCTGAAGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCAGCGGCGACTGTGGGCAACATCGAGAGCTGGCTGCTGAATGAAGAGTGCGAGGTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAlaAspIleCysIleAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCCCGGCTGACACCTGCTCTCAGGAGCAGCACCAGTGGTGGAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCATGTCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGACGATGGGACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCCACCAAGTATCCGCTCATCGCTGACAGAGGACTG 651

RESULT 9
US-10-063-512-127
; Sequence 127, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-127

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-512-127 (1-1505)

Qy 1 MetAlaArgProGlyMetGluAtrGTPArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCGCGCATGGAGCGGTGGCGGACCGGCTGGCGCTGGAGCGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaValAlaAraGAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGGCGCGCGTGGCCCGGCGCTGGTCCAGCAGGAGCTGAAGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCAGCGGCGACTGTGGGCAACATCGAGAGCTGGCTGCTGAATGAAGAGTGCGAGGTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAlaAspIleCysIleAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCCCGGCTGACACCTGCTCTCAGGAGCAGCACCAGTGGTGGAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCATGTCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGACGATGGGACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCCACCAAGTATCCGCTCATCGCTGACAGAGGACTG 651
```

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Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCGGGGCTGACACCCCTGCTCTAGGAGCAGCACCAGTGGTTGGAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTrpGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACAGGGAAGCCTACCAAGTCCATGAAGAGCGGAT 531
Qy 141 ValAspAspGlyHisIleLeuAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATCCCTG 591
Qy 161 SerValThrHisPheThrSerAlaThrLysTrpAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCCACCMAGTATGCCGTGCTGCTGACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGCAAGAGCTTCCGGAGGCCACACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
Db 712 GTGGAGACACAATTCGGCTTCAAACTCCACAGGAGCCCTGGAAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAATGAAGTGTCTCAACCCGAGGATGTGGCCGAGGCTGTTATCTAGTCTCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCGGAGCGAGTGTACC 891
```

RESULT 10

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US-10-063-513-127
; Sequence 127, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-127
```

Alignment Scores:

```
Pred. No.: 1,83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
```

US-10-063-735-128 (1-260) x US-10-063-513-127 (1-1505)

```
Qy 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGGCCAGGCGCGCATGAGCGGTGGCGGACCGGCTGGTGTACGCGGCGCTCG 171
```

```
Qy 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGCGCGCGCGCTGCGCCGGGCCCTGTGTCCAGCAGGAGCTGAAGGTGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCCCGGCATGTGGGCAACATCAGAGAGCTGCTGCTGAATGTGAAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTTGATCCCTTACAGATGTGACCATCAAAATGAAGAGGACATCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCCTTCTCAGCACAGCGGTGAGACATCTGCATCAACATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCGCGGCTGACACCCCTGCTCTCAGGAGCAGCACCAGTGGTTGGAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTrpGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACAGGGAAGCCTACCAAGTCCATGAAGAGCGGAA 531
Qy 141 ValAspAspGlyHisIleLeuAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATCCCTG 591
Qy 161 SerValThrHisPheThrSerAlaThrLysTrpAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTGCTGCTGACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGCAAGAGCTTCCGGAGGCCACACCCACATCCAGGCCAGTGCATCTCTCCAGGTGTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
Db 712 GTGGAGACACAATTCGGCTTCAAACTCCACAGGAGCCCTGGAAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAATGAAGTGTCTCAACCCGAGGATGTGGCCGAGGCTGTTATCTAGTCTCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCGGAGCGAGTGTACC 891
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RESULT 11

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US-10-063-569-127
; Sequence 127, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
```

US-10-063-569-127

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-569-127 (1-1505)

```
QY 1 MetAlaArgProGlyMetGluAArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
DB 112 ATGCCAGGCCCGCGCATGGAGCGGTGGCGGACCGGCTGGCTGGTGCAGCGGGGCTCG 171
QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuValValGly 40
DB 172 GGGGGCATCGCGCGCGCGGTGGCGCGGCTGGTCCAGCAGGAGCTGAAGGTGGTGGC 231
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
DB 232 TGGCGCGGCTGTGGCAACATCGAGAGCTGGCTGCTGAATGAAGAGTGCAGGCTAC 291
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
DB 292 CCCGGGACTTGTATCCCTACAGATGTGACTATCAAAATGAAGAGGACATCTCTCCATG 351
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
DB 352 TTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTG 411
QY 101 AlaArgProAspThrLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
DB 412 GCCCGGCTGACACCTGCTCTCAGGAGCAGCAGTGGTGGAGAGGACATGTTCAATGTG 471
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
DB 472 AACGTGCTGGCTCTCAGCATCTGCACACGCGGAGCTTACCAGTCCATGAAGAGCGGAAT 531
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
DB 532 GTGGAGCATGGGCACATCAATTAACATCAATAGCATGTCTGCCACCGAGTGTATCCCTG 591
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
DB 592 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCGCTCAGTGCAGAGGAGCTG 651
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
DB 652 AGCAAGAGCTTCGGAGGCGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
DB 712 GTGGAGACACAATTCGCTTCAAACTCCACGCAAGGACCTGAGAAGGCGAGCTGCCACC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
DB 772 TATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTATCTACGCTCT 831
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
DB 832 AGCACCCCGCACACATCCAGATTTGAGACATCCAGATGAGGCCCCCGAGGAGGTGACC 891
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RESULT 12

US-10-063-551-127
; Sequence 127, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-127

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-551-127 (1-1505)

```
QY 1 MetAlaArgProGlyMetGluAArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
DB 112 ATGCCAGGCCCGCGCATGGAGCGGTGGCGGACCGGCTGGCTGGTGCAGCGGGGCTCG 171
QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuValValGly 40
DB 172 GGGGGCATCGCGCGCGCGGTGGCGCGGCTGGTCCAGCAGGAGCTGAAGGTGGTGGC 231
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
DB 232 TGGCGGCTGACACCTGCTCTCAGGAGCAGCAGTGGTGGAGAGGACATGTTCAATGTG 291
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
DB 292 CCCGGGACTTGTATCCCTACAGATGTGACTATCAAAATGAAGAGGACATCTCTCCATG 351
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
DB 352 TTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTG 411
QY 101 AlaArgProAspThrLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
DB 412 GCCCGGCTGACACCTGCTCTCAGGAGCAGCAGTGGTGGAGAGGACATGTTCAATGTG 471
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
DB 472 AACGTGCTGGCTCTCAGCATCTGCACACGCGGAGCTTACCAGTCCATGAAGAGCGGAAT 531
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
DB 532 GTGGAGCATGGGCACATCAATTAACATCAATAGCATGTCTGCCACCGAGTGTATCCCTG 591
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
DB 592 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCGCTCAGTGCAGAGGAGCTG 651
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
DB 652 AGCAAGAGCTTCGGAGGCGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
DB 712 GTGGAGACACAATTCGCTTCAAACTCCACGCAAGGACCTGAGAAGGCGAGCTGCCACC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
```

Db 772 TATGAGCAATGAAGTGTCTCAACCCGAGGATGTGGCCGAGGCTGTATCTAGTCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGGTGACC 891
RESULT 13
US-10-174-581-377
; Sequence 377, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Denoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22

1	PRIOR APPLICATION NUMBER: 60/087099
2	PRIOR FILING DATE: 1998-05-28
3	PRIOR APPLICATION NUMBER: 60/087208
4	PRIOR FILING DATE: 1998-05-28
5	PRIOR APPLICATION NUMBER: 60/087609
6	PRIOR FILING DATE: 1998-06-02
7	PRIOR APPLICATION NUMBER: 60/087759
8	PRIOR FILING DATE: 1998-06-02
9	PRIOR APPLICATION NUMBER: 60/087827
10	PRIOR FILING DATE: 1998-06-03
11	PRIOR APPLICATION NUMBER: 60/088025
12	PRIOR FILING DATE: 1998-06-04
13	PRIOR APPLICATION NUMBER: 60/088028
14	PRIOR FILING DATE: 1998-06-04
15	PRIOR APPLICATION NUMBER: 60/088029
16	PRIOR FILING DATE: 1998-06-04
17	PRIOR APPLICATION NUMBER: 60/088033
18	PRIOR FILING DATE: 1998-06-04
19	PRIOR APPLICATION NUMBER: 60/088167
20	PRIOR FILING DATE: 1998-06-05
21	PRIOR APPLICATION NUMBER: 60/088202
22	PRIOR FILING DATE: 1998-06-05
23	PRIOR APPLICATION NUMBER: 60/088212
24	PRIOR FILING DATE: 1998-06-05
25	PRIOR APPLICATION NUMBER: 60/088217
26	PRIOR FILING DATE: 1998-06-05
27	PRIOR APPLICATION NUMBER: 60/088326
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088655
30	PRIOR FILING DATE: 1998-06-09
31	PRIOR APPLICATION NUMBER: 60/088722
32	PRIOR FILING DATE: 1998-06-10
33	PRIOR APPLICATION NUMBER: 60/088738
34	PRIOR FILING DATE: 1998-06-10
35	PRIOR APPLICATION NUMBER: 60/088740
36	PRIOR FILING DATE: 1998-06-10
37	PRIOR APPLICATION NUMBER: 60/088911
38	PRIOR FILING DATE: 1998-06-10
39	PRIOR APPLICATION NUMBER: 60/088924
40	PRIOR FILING DATE: 1998-06-10
41	PRIOR APPLICATION NUMBER: 60/088925
42	PRIOR FILING DATE: 1998-06-10
43	PRIOR APPLICATION NUMBER: 60/088926
44	PRIOR FILING DATE: 1998-06-10
45	PRIOR APPLICATION NUMBER: 60/088961
46	PRIOR FILING DATE: 1998-06-11
47	PRIOR APPLICATION NUMBER: 60/088963
48	PRIOR FILING DATE: 1998-06-11
49	PRIOR APPLICATION NUMBER: 60/088976
50	PRIOR FILING DATE: 1998-06-11
51	PRIOR APPLICATION NUMBER: 60/089090
52	PRIOR FILING DATE: 1998-06-12
53	PRIOR APPLICATION NUMBER: 60/089105
54	PRIOR FILING DATE: 1998-06-12
55	PRIOR APPLICATION NUMBER: 60/089512
56	PRIOR FILING DATE: 1998-06-16
57	PRIOR APPLICATION NUMBER: 60/089514
58	PRIOR FILING DATE: 1998-06-16
59	PRIOR APPLICATION NUMBER: 60/089538
60	PRIOR FILING DATE: 1998-06-17
61	PRIOR APPLICATION NUMBER: 60/089598
62	PRIOR FILING DATE: 1998-06-17
63	PRIOR APPLICATION NUMBER: 60/089653

; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-483-377

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-176-483-377 (1-1505)

```
Qy 1 MetAlaArgProGlyMetGluArgTrrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCGCGCATGGAGCGGTGGCGCGACCGCGCTGGGTGACGGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCGCCCGCATCTGGGCAACATCAGAGCTGGCTGCTGAATGTAAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAlaPileLeuSerMet 80
Db 292 CCGCGGACTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrrLysAspMetPheAsnVal 120
Db 412 GCCCGCGCGCATGACCCCTCTCTCAGGCGAGCACCAGTGGTTGGAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCGCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleAlaPheLysLeuHisAspLysAspProGlyLysAlaAlaThr 160
Db 532 GTGGAGCATGGGCACATCATTAACATCAATAGCATGTCTGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrIlystTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTCCACCAAGATGATGCCGTCACTGGCGCTGACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAGAGCTTTCGGAGGCGCCAGACCCACATCCGAGCCAGCTGTCATCTCCAGGTTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGlyLysAlaAlaThr 220
Db 712 GTGGAGACACAATTCGCCTTCAAACTCCACCAAGGACCTTGAGAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCCGAGATGTGCCGAGGTGTTATCTAGCTCCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACC 891
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RESULT 15

US-10-176-749-377

; Sequence 377, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-377

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-176-749-377 (1-1505)

```
Qy 1 MetAlaArgProGlyMetGluArgTrrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCGCGCATGGAGCGGTGGCGCGACCGGTGGCGCTGGGTGACGGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCGCCCGCATCTGGGCAACATCAGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAlaPileLeuSerMet 80
Db 292 CCGCGGACTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrrLysAspMetPheAsnVal 120
Db 412 GCCCGCGCGCATGACCCCTCTCTCAGGCGAGCACCAGTGGTTGGAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCGCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleAlaPheLysLeuHisAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGAGCATGGGCACATCATTAACATCAATAGCATGTCTGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrIlystTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTCCACCAAGATGATGCCGTCACTGGCGCTGACAGAGGACTG 651
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Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
Db	652	AGGCAAGAGCTTCGGAGGCCAGACCACATCGAGCCACGTGCATCTCTCCAGGTGTG	711
Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr	220
Db	712	GTGGAGACACAATTGCGCTTCAAACTCCACGACAAGGACCTGAGAAGGCAGCTGCCACC	771
Qy	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240
Db	772	TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTATCTAGTCCTC	831
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260
Db	832	AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCCACGGAGCGGTGACC	891

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